

responses and effects on K^+ channels, may be performed in living cells, broken cells, isolated cell membranes, as well as in tissues and in living animals. To facilitate measurement of physiological GABA_B receptor mediated responses, GABA_B receptors may be co-expressed with promiscuous G-proteins like e.g. G α 16 or Gq15 increasing G-protein coupling. Another possible way to increase G-protein coupling is to fuse the GABA_B receptor with appropriate G-proteins using standard molecular techniques. In order to further improve readouts in Ca^{++} -response assays, GABA_B receptors may be co-expressed with aequorin, a photoprotein cloned from the luminescent jellyfish *Aequorea victoria*.

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In yet another aspect, the invention provides a pharmaceutical compositions comprising a soluble GABA_B receptor further comprising one or more pharmaceutical acceptable carriers and/or diluents.

15 In yet another aspect, the invention provides a method for the diagnosis or treatment of conditions related to GABA-dysfunction, e.g. epilepsy, psychiatric disorders such as depression and anxiety, cognitive dysfunction, gastroesophageal reflux disease, emesis, irritable bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune diseases, neoplastic diseases, pain, and infectious diseases, comprising the use or administration of soluble forms of the GABA_B receptor, such as the human GABA_B receptor 1c or 1d or functionally equivalent modified forms thereof; preferably being a polypeptide of the present invention..

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The soluble forms of the GABA_B receptor can e.g. be produced by culturing a host cell harbouring a vector comprising a nucleic acid encoding the soluble GABA_B receptor under conditions where whereby the said polypeptide is produced, the polypeptide recovered and administered to a patient in need thereof.

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30 Furthermore, the level of soluble GABA_B receptors in certain body fluids, e.g. serum and CSF, can be measured and used in diagnostics related to conditions with altered levels of soluble GABA_B receptors in said body fluids.

Throughout this description the terms "standard protocols" and "standard procedures", when used in the context of molecular cloning techniques, are to be understood as protocols and procedures found in an ordinary laboratory manual such as: Current Protocols in Molecular Biology, editors F. Ausubel et al., John Wiley and Sons, Inc. 1994, or Sambrook, J., Fritsch, E.F. and Maniatis, T., Molecular Cloning: A laboratory manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY 1989.

EXAMPLES

EXAMPLE 1A: Cloning and sequencing of cDNA encoding human GABA_B receptor 1a and 1b

Messenger RNA from human hippocampus was obtained from Clontech (Palo Alto, CA, USA) (catalog #6578-1). First-strand cDNA synthesis reactions were performed using the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The pd(N)₆ primer was used to prime the first-strand synthesis. The generated cDNA molecules were used as template in the PCR reactions described below.

Specific PCR primers were designed (Table 1) based on the sequences of the rat GABA_B receptor 1a and 1b cDNA (Kaupmann et al. 1997, EMBL accession numbers Y10369 (SEQ ID NO: 44) and Y10370 (SEQ ID NO: 46)).

TABLE 1

Primers used for RT-PCR on mRNA from human hippocampus

Nr.	Species	Sequence 5' - 3'	SEQ ID NO
794	Rat	GTTTCTTCTCGGATCCAGCTGTGCCTG	1
795	Rat	CAGGCACAGCTGGATCCGAGAAGAACT	2
796	Rat	CGGTCGACTCACTTGTAAGCAAATGTACTCGACTCCC	3
797	Rat	ATGCGCGCCGCGCAGCCAACATGCTGCTGCTGCTGCTGGTGC	4
831	Rat	CGGTCGACTCACTTGTAAGCAAATGTACTCGACTCCCATCACAGC	5
838	Rat	ATGCGCGCCGCGCAGCCAACATGCTGCTGCTGCTGCTGGTGCCTCTCTTCC	6
842	Rat	CAGGCACAGCTGGATCCGAGAAGAACTCTGTGCGAAAGT	7
863	Rat	GGTCATCCAGCGTTGAGGTGAAGAC	8
864	Rat	GAAGGTTGCCAGATTATACATCCGC	9
865	Rat	CCACGATGATTCGAGCATCTTGACG	10
866	Rat	GCCTCTCACTCCCCTCATCTCC	11
932	Human	GAGTGAAGGAGGCTGGAATTG	12

- 5 cDNA fragments encoding parts of the human GABA_B receptors were amplified directly by PCR using the designed primers with the generated cDNA molecules as templates. All PCR experiments were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: +95°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes, repeated 44 times and finally
- 10 +72°C for 7 minutes. The following primer combinations gave PCR products with expected sizes: 838 and 842, 838 and 795, 797 and 865, 864 and 865, 864 and 863 which corresponds to the 5'-end of the GABA_B receptor 1a. Primer pair 932 and 831, 932 and 796, 794 and 831 gave PCR products which correspond to the 3'-end of both GABA_B receptor 1a and 1b. The primer combination 839 and 918 gave a PCR product
- 15 corresponding to the 5'-end of the GABA_B receptor 1b.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator

20 cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA_B receptor were used.

Additional PCR primers were designed based on the obtained sequences encoding fragments of the human GABA_B receptor and additional DNA fragments encoding parts of the human GABA_B receptors were amplified by PCR, the PCR products subcloned and
5 sequenced as described above.

EXAMPLE 1B : Cloning and sequencing of the 3'-ends of the cDNA encoding human GABA_B receptors 1a and 1b

10 Messenger RNA from human hippocampus was obtained from Clontech (Palo Alto, CA, USA) (catalogue #6578-1). First strand cDNA synthesis reactions were performed using the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The Not I-d(T)₁₈ primer was used to prime the first-strand synthesis. The
15 generated cDNA molecules were used as template in the PCR reactions described below.

Specific PCR primers were designed (Table 2) based on the sequences of the human GABA_B receptor 1a and 1b cDNA obtained in Example 1A and the EST sequence EMBL accession number Y11044.

20 By homology searches in the EMBL database using the GABA_B receptor cDNA sequences obtained in Example 1A as query the EST sequence EMBL accession number Y11044 have been found to be homologous to the 3'-end of the GABA_B receptor cDNA.

25 TABLE 2

Primers used in PCR to amplify 3'ends of human GABA_B receptor cDNA

Nr	Species	Sequence 5'-3'	SEQ ID NO
938	Human	GACGCTTATCGAGCAGCTTC	13
972	Human	AGCCAGAACTCACAGGGGGACAT	14
973	Human	GCTCAAGCCAGGTACGAAGTAA	15

cDNA fragments encoding parts of the human GABA_B receptors were amplified directly by
30 PCR using the designed primers with the generated cDNA molecules as templates. All

PCR experiments were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: + 95°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes, repeated 44 times and finally +72°C for 7 minutes. The following primer combinations gave PCR products with expected sizes: 938 and 972, 938 and 973 corresponding to the 3' end of both GABA_B receptor 1a and 1b cDNA.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA_B receptor were used.

EXAMPLE 1C : Cloning and sequencing of the 5'-end of the cDNA encoding human GABA_B receptor 1b

Messenger RNA from human hippocampus was obtained from Clontech (Palo Alto, CA, USA) (catalogue #6578-1). Marathon cDNA amplification Kit (Clontech) was used for performing 5'/3' - RACE (Rapid Amplification of cDNA Ends). Adaptor-ligated double stranded cDNA molecules were amplified according to the manufacturers description. The pd(N)₆ primer from the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden) was used to produce the adaptor-ligated cDNA.

A specific PCR primer was designed (Table 3) based on the sequences of the human GABA_B receptor 1b cDNA obtained in Example 1A.

TABLE 3

Primers used in PCR to amplify the 5'-ends of human GABA_B receptor cDNA

Nr.	Species	Sequence 5'-3'	SEQ ID NO
958	Human	TGGCCCTCCACCGCCTCAGTCATCTCA	16
AP1	Marathon kit	CCATCCTAATACGACTCACTATAGGGC	17

5 cDNA fragments encoding part of the human GABA_B receptors were amplified directly by PCR using the designed primers with the generated adaptor-ligated cDNA molecules as template. The PCR experiment was carried out using the Expand Long Template PCR System (Boehringer Mannheim GmbH, Germany) with the following PCR program: + 94°C for 1minute, + 94°C for 30 seconds, +60°C for 30 seconds, +68°C for 4 minutes, repeated 24 times. The primer combination AP1 and 958 gave a PCR product which
10 corresponded to the 5'-end of the GABA_B receptor 1b cDNA, including 190 base pairs upstream the initiation codon.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide
15 sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA_B receptor were
20 used.

EXAMPLE 1D : Cloning and sequencing of the 5'-end of the cDNA encoding human GABA_B receptor 1a

25 Messenger RNA from human hippocampus was obtained from Clontech (Palo Alto, USA) (catalogue #6578-1). Marathon cDNA amplification Kit (Clontech) was used to obtain adaptor-ligated double stranded cDNA molecules according to the manufacturer's description. The pd(N)₆ primer from the First-strand cDNA Synthesis kit from Amersham
30 Pharmacia Biotech (Uppsala, Sweden) was used to obtain the adaptor-ligated cDNA .

Specific PCR primers were designed (Table 4) based on the sequences of the human GABA_B receptor 1a cDNA obtained in Example 1 and the rat GABA_B receptor 1a cDNA disclosed in WO 97/46675.

TABLE 4

Primers used to amplify 5'-ends of the human GABAB receptor 1a cDNA

Nr.	Species	Sequence 5'-3'	SEQ ID NO
1033	Human	CTCAATCTCATAGTCCACTGG	18
1087	Rat	CCTTGAGGCCCGGGGAGAG	19

- 10 cDNA fragments encoding part of the human GABAB 1a receptor were amplified directly by PCR using the designed primers with the generated adaptor-ligated cDNA molecules as template. The PCR was performed using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: +94°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes; +94°C for 1 minute, +60°C
15 for 30 seconds, +72°C for 4 minutes, repeated 34 times and finally +72°C for 7 minutes.

The primer combination 1087 and 1033 gave a PCR product corresponding to the 5'-end of the GABA_B receptor 1a cDNA, including 26 base pairs upstream the initiation codon.

- 20 The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As
25 primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T were used.

- A complete cDNA sequence encoding the human GABA_B receptors 1a (SEQ ID NO: 48) and the human GABA_B receptor 1b (SEQ ID NO: 50) were obtained by aligning the sequences of the different fragments cloned and sequenced in Examples 1A, 1B, 1C and
30 1D.

EXAMPLE 2A: Cloning and sequencing of cDNA encoding canine GABA_B receptor 1a

- 5 QuickPrep Micro mRNA Purification kit (Amersham Pharmacia Biotech, Uppsala, Sweden) was used to isolate mRNA from canine neural tissues according to the manufacturers description. First-strand cDNA synthesis reactions were performed using the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The Not-I-d(T)₁₈ bifunctional or pd(N)₆ primer was used to prime the first-strand synthesis.
- 10 The generated cDNA molecules were used as template in the PCR reactions described below.

Specific PCR primers (Table 5) were designed based on the sequences of the rat GABA_B receptor 1a and 1b cDNA (Kaupmann et al. 1997, EMBL accession numbers Y10369 (SEQ ID NO: 44 and Y10370 (SEQ ID NO: 46)).

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TABLE 5

Primers used for RT-PCR on mRNA from canine cortex

Nr.	Species	Sequence 5'-3'	SEQ ID NO
795	Rat	CAGGCACAGCTGGATCCGAGAAGAAACT	20
831	Rat	CGGTCGACTCACTTGTAAGCAAATGTACTCGACTCCCATCACAGC	21
838	Rat	ATGCGCGCCGGCAGCCAACATGCTGCTGCTGCTGCTGGTGCCTCTCTTCC	22
840	Rat	CGTCAAGATGCTCGAATCATCG	23
841	Rat	CAGGGGGCTCAGAGGGTCCC	24
842	Rat	CAGGCACAGCTGGATCCGAGAAGAAACTCTGTCCGAAAGT	25
844	Rat	CGGTCGACTCACTTGTAAGCAAATGTACTCGACTCCCATCACAGCTAAG	26
848	Rat	ACTTTCCGACAGAGTTTCTTCTCGGATCCAGCTGTGCCTG	27
865	Rat	CCACGATGATTCGAGCATCTTGACG	28

20 cDNA fragments encoding parts of the canine GABA_B receptor were amplified directly by PCR using the designed primers with the generated cDNA molecules as templates. All PCR experiments were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: +95°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes, repeated 44 times and finally

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+72°C for 7 minutes. The following primer combinations gave PCR products with expected sizes: 842 and 838, 838 and 795, 838 and 865 which corresponds to the 5'-part of the canine GABA_B receptor cDNA. Primer pair 848 and 844, 848 and 831, 848 and 841, 840 and 841 gave PCR products which correspond to the 3'-part of the canine GABA_B receptor cDNA.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA_B receptor were used.

EXAMPLE 2B: Cloning and sequencing of the 3'- and 5'-ends of the cDNA encoding canine GABA_B receptor 1a

QuickPrep Micro mRNA Purification kit (Amersham Pharmacia Biotech, Uppsala, Sweden) was used to isolate mRNA from canine nerve tissues according to the manufactures description. Marathon cDNA amplification Kit (Clontech, Palo Alto, CA, USA) were used for performing both 5'-and 3'-RACE. Two adaptor-ligated double stranded cDNA libraries were amplified according to the manufacturers description. A random primer (pd(N)₆) was used when amplifying the adaptor-ligated cDNA for the 5'-RACE and the Marathon cDNA Synthesis primer (52-mer) was used when amplifying the adaptor ligated cDNA for the 3'-RACE.

Specific PCR primers were designed (Table 6) based on the sequence of canine GABA_B receptor 1a cDNA obtained in Example 2A.

TABLE 6

Primers used in PCR to amplify the 5'- and 3'-ends of canine GABA_B receptor 1a cDNA

Nr.	Species	Sequence 5'-3'	SEQ ID NO
936	canine	CTACCGCGCAATGAACTCCTCGTC	29
1076	canine	CGAGGTGGCGTTGGGGGTCTGTGC	30
AP1	Marathon kit	CCATCCTAATACGACTCACTATAGGGC	31
AP2	Marathon kit	ACTCACTATAGGGCTCGAGCGGC	32

5 cDNA fragments encoding parts of the canine GABA_B receptor were amplified by PCR from the adaptor-ligated cDNA using the designed primers. A number of different PCR programs were tested to find conditions where PCR products corresponding to GABA_B receptor DNA were obtained. The 5'- PCR experiments were carried out using the Expand Long Template PCR System (Boehringer Mannheim GmbH, Germany) with the following
 10 PCR program: +94°C for 30 seconds, +72°C for 3 minutes, repeated 4 times; +94°C for 30 seconds, +70°C for 3 minutes, repeated 4 times; and +94°C for 30 seconds, +68°C for 3 minutes, repeated 24 times. The primer combination AP2 and 1076 gave a PCR product which corresponded to the 5'-end of the GABA_B receptor cDNA, including 114 base pairs upstream the initiation codon.

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The 3'- PCR experiments were carried out using the Expand Long Template PCR System (Boehringer Mannheim GmbH, Germany) with the following PCR program: +94°C for 1 minute; and +94°C for 30 seconds, +60°C for 30 seconds, +68 °C for 4 minutes, repeated
 20 to the 3'-end of the GABA_B receptor cDNA, including the poly(A) tail.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator
 25 cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to GABA_B receptor DNA were used.

Complete cDNA sequence encoding the canine GABA_B receptor 1a (SEQ ID NO: 52) was obtained by aligning the sequences of the different fragments obtained in Example 2A and Example 2B.

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EXAMPLE 3A: Cloning of cDNA encoding human GABA_B receptor 1c and 1d from Jurkat cells

A guanidinisothiocyanate/CsCl method was used to isolate total RNA from Jurkat cells.

10 The first-strand cDNA synthesis was performed using the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The pd(N)₆ primer was used to prime the first strand synthesis. The generated cDNA molecules were used as templates in the PCR reaction described below.

15 Specific PCR primers (Table 7) were designed based on the sequence of human GABA_B receptor 1a and 1b cDNA (Example 1), rat GABA_B receptor (Kaupmann et al. 1997) and the EST sequence EMBL accession number Y11044.

TABLE 7

20 Primers used in RT-PCR on mRNA from Jurkat cells

Nr	Species	Sequence 5'-3'	SEQ ID NO
938	human	GACGCTTATCGAGCAGCTTC	33
972	human	AGCCCAGAACTCACAGGGGGACAT	34
973	human	GCTTCAAGCCAGGTACGAACTAA	35
893	rat	GGAGCACCCCCAAGCCCCACTG	36
937	human	CTGGTTCCTCCCAATGTG	37
1005	rat	CCTCTCACTCCCCTCATCTC	38
1030	human	AAGCCAACCTTCCCTGCTTCTC	39

cDNA fragments encoding parts of the GABA_B receptor were amplified directly by PCR using human and rat specific primers. All PCR experiments were carried out using the

25 Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ,

USA) with the following PCR program: +95°C for 1 minute; +54°C for 1 minutes, +72°C for 3 minutes, repeated 44 times; and finally +72°C for 7 minutes.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to GABA_B receptor DNA were used.

The following primer combination gave PCR products corresponding to the 3'-end of the GABA_B receptor cDNA: primer pairs 938 and 972; 938 and 973. Unexpectedly both these fragments lacked 149 base pairs, resulting in a frame shift and the insertion of a new termination codon. The following primer combination gave a PCR product corresponding to the 5'-part of the GABA_B receptor 1a cDNA: 893 and 937. The primer pairs 1005 and 937, 1030 and 937 gave PCR products corresponding to the 5'-part of the GABA_B receptor 1b cDNA. Also these PCR fragments lacked the same 149 base pairs which resulted in a frame shift and the insertion of a new termination codon.

These results show that Jurkat cells contain mRNA encoding two new forms of the human GABA_B receptor. These are designated GABA_B receptor 1c (SEQ ID NO: 54 and 55) (comprising the same 5'-part as the GABA_B receptor 1a) and GABA_B receptor 1d (SEQ ID NO: 56 and 57) (comprising the same 5'-part as the GABA_B receptor 1b). These two forms of the GABA_B receptor do not contain any of the transmembrane regions and are therefore expected to be soluble forms of the receptor.

EXAMPLE 3B: Analysis of cDNA encoding human GABA_B receptors from hippocampus

Messenger RNA from human hippocampus was obtained from Clontech (Palo Alto, USA) (catalogue #6578-1). First strand cDNA synthesis reactions were performed using the First-strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The

pd(N)₆ primer was used to prime the first-strand synthesis. The generated cDNA molecules were used as template in the PCR reactions described below.

Specific PCR primer was designed (Table 8) based on the sequences of the cDNAs encoding human GABA_B receptors 1a and 1b.

TABLE 8

Primers used for RT-PCR on mRNA from human hippocampus

Nr	Species	Sequence 5' - 3'	SEQ ID NO
937	Human	CTGGTTCCTCCCAATGTG	40
938	Human	GACGCTTATCGAGCAGCTTC	41

cDNA fragments encoding parts of the human GABA_B receptors were amplified directly by PCR using the designed primers with the generated cDNA molecules as templates. All PCR experiments were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: +94°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes; +94°C for 1 minute, +54°C for 30 seconds, +72°C for 3 minutes repeated 44 times; and finally +72°C for 7 minutes. The primer combination 938 and 937 gave a PCR product which corresponded to the expected size of the GABA_B receptor 1a and 1b cDNA but also a fragment a smaller size.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA_B receptor were used.

The larger PCR fragment was found to correspond to the 3'-part of the GABA_B receptor 1a and 1b cDNA and the smaller fragment which lacked 149 base pairs was found to correspond to the 3'-part of the GABA_B receptors 1c and 1d cDNA identified in Example 3A.

EXAMPLE 4: Cloning and sequencing of cDNA encoding canine GABA_B receptor 1b

cDNA encoding the canine GABA_B receptor 1b is isolated in a similar manner as described in Example 2 for receptor 1a. PCR primers specifically designed to be complementary to the 5'-end of the cDNA encoding the rat and human GABA_B receptor 1b, together with PCR primers complementary to the 3'-end of the cDNA encoding the canine GABA_B receptor 1a, and mRNA prepared from a suitable canine tissue, are used.

EXAMPLE 5: Cloning of cDNA encoding canine GABA_B receptor 1c

Total RNA from canine liver was prepared using the RNeasy Total RNA Purification Protocols (Quiagen GmbH, Germany). The first-strand cDNA synthesis was performed using the First-strand cDNA Synthesis kit from (Amersham Pharmacia Biotech, Uppsala, Sweden). The pd(N)₆ primer was used to prime the first -strand synthesis. The generated cDNA molecules were used as templates in the PCR reaction described below.

Specific PCR primers (Table 9) were designed based on the sequence of canine GABA_B receptor 1a cDNA.

TABLE 9**Primers used in RT-PCR**

Nr	Species	Sequence 5'-3'	SEQ ID NO
936	canine	CTACCGCGCAATGAACTCCTCGTC	42
954	canine	CCTTCTTCTCCTCCTTCTTAGTGA	43

cDNA fragments encoding parts of the canine GABA_B receptor were amplified directly by PCR using canine specific primers. All PCR experiments were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular Systems Inc., NJ, USA) with the following PCR program: +95°C for 1 minute, +54°C for 30 seconds, +72°C for 3

minutes, repeated 44 times and finally +72°C for 7 minutes. The primer combination gave a PCR product with a size corresponding to the GABA_B receptor 1a but also a fragment of smaller size indicating the presence of a GABA_B receptor 1c.

5 The PCR products were subcloned into the pGEM-T vector from Promega (Madison, USA). The inserts were subjected to nucleotide sequence analysis, the complete nucleotide sequence for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to the vector
10 pGEM-T were used.

The smaller fragment was shown to lack 149 base pairs. This deletion caused a frame shift and an insertion of a new termination codon, verifying the existence of a canine GABA_B receptor 1c.

15 Complete cDNA sequence encoding the canine GABA_B receptor 1c (SEQ ID NO: 58) was obtained by aligning the sequences of the fragments obtained in Example 2A, Example 2B and Example 5.

20 **EXAMPLE 6. Cloning, sequencing and organization of human GABA_B receptor genomic fragments**

To determine the structural organization and sequence of the human GABA_B receptor gene,
25 human genomic DNA libraries and human genomic DNA were screened and analyzed. Human genomic libraries were obtained from Clontech (Palo Alto, CA, USA). The libraries were constructed from female leukocyte DNA (catalog # HL1111J), cloned into λEMBL-3 vector. The average size of inserts are 16 kb and the number of independent clones are 1.7×10^6 . Human genomic DNA was obtained from Clontech (catalog # 6550-1).

30 In order to isolate recombinant phages containing exon and intron sequences of the human GABA_B receptor gene, 48 individual bacterial plates with a diameter of 150 mm and approximately 4×10^4 individual plaques per plate, were screened. The methods and

solutions used were as described in the Library Protocol Handbook: General Procedures for the Hybridization of Lambda Phage Libraries w/DNA Probes (Clontech) with some modifications as will be apparent from the following.

- 5 The experiment was carried out essentially as follows. The numbers are given per plate basis. A sample of the phage library diluted in 0.1 ml sterile lambda diluent was prepared in order to obtain an estimated titer of 40,000 pfu (plaque forming units). A 0.6 ml LB-medium culture of the *E. coli* host strain K802 (obtained from Clontech) was infected with 40000 pfu recombinant phages for 15 minutes at +37°C. The culture was then mixed with
10 7 ml top agarose (6.5 g of agarose added per liter LB) and poured onto LB plates. The plates were incubated at +37°C for approximately 7 hours. The plates were then chilled at +4°C.

- Plaque hybridization experiments were as follows. Membrane filters, Colony/Plaque
15 Screen (DuPont, Wilmington, DE, USA), were placed onto the top of the plates for 3 minutes. For denaturation of DNA the filters were removed and floated in 0.5 M NaOH on a plastic wrap for 2 minutes, with the plaque side up. This step was repeated once to ensure efficient denaturation. Following neutralization the membrane filters were placed in 1M Tris-HCl pH 7.5, two times 2 minutes and allowed to dry.

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- To obtain probes for DNA hybridization screening of the membrane filters, a GABA_B receptor cDNA clone was digested with SacII and a 479 bp fragment (base pairs 573-1051 in the cDNA encoding human GABA_B receptor 1a, SEQ ID NO: 48) was separated by agarose electrophoresis, excised and transferred to a polypropylene microcentrifuge tube.
25 Additional probes were obtained by PCR amplification of various regions of the GABA_B receptor cDNA (base pairs 68-486 and 2368-2863 in the cDNA encoding human GABA_B receptor 1a, SEQ ID NO: 48). The isolated cDNA fragment was ³²P-labeled using Megaprime DNA labeling system (Amersham Pharmacia Biotech, Uppsala, Sweden) by the following procedure. Water was added at a ratio of 3 ml per gram of gel, and placed in
30 a boiling water bath for 7 minutes to melt the gel and denature the DNA. A volume of DNA/agarose solution containing 25 ng of DNA was added to the labeling reaction, according to the supplier's instructions. Labeled nucleotides were removed from DNA

labeling reactions using MicroSpin™ G-50 Columns (Amersham Pharmacia Biotech, Uppsala, Sweden).

The DNA hybridization reaction was performed under stringent conditions according to the method described below. The filter membranes were prehybridized at +65°C for at least 1 hour in a solution composed of 1% SDS, 1M NaCl, and 10% dextran sulfate using a hybridization oven (Hybaid Ltd, Ashford, UK). Following prehybridization a solution containing denatured herring sperm DNA of a final concentration of 100 µg/ml and the ³²P-labeled DNA probe at a concentration <10 ng/ml (for optimal signal to background ratio) was added to the prehybridization solution and the membrane filters were incubated at +65°C for 10-20 hours. Following the removal of the hybridization solution the membrane filters were first washed in a 2xSSC (0.3M NaCl, 0.03M Na-citrate), 1% SDS solution two times for 5 minutes at room temperature. In the next step, the membrane filters were incubated +60°C two times for 30 minutes each in the same solution. In a third step, the filters were washed two times at room temperature in 0.1xSSC. Finally, the membrane filters were placed on a sheet of filter paper with the DNA face up, and allowed to dry. The dried membrane filters were then exposed to X-ray films and autoradiographed.

Of the approximately 2x10⁶ individual plaques analyzed, four hybridizing plaques were detected and isolated. These three isolates were designated #GR1, #GR12, #GR13 and #GR41, respectively. After several rescreening experiments, the recombinant phage DNA was purified using Qiagen Lambda Midi Kit (Qiagen GmbH, Germany). The purified DNA was digested with SalI and the fragments representing the inserts were isolated by agarose electrophoresis.

The sizes of the inserts were approximately isolate #GR1, 12 kb, isolate #GR12, 12 kb; isolate #GR13, 16kb; and isolate #GR41, 19 kb. These fragments were cloned into SalI digested linearized pUC19, resulting in the plasmids pAM362 (isolate #GR1), pAM363 (isolate #GR12), pAM364 (isolate #GR13) and pAM365 (isolate #GR41). The inserts from the four plaques which hybridizes to the GABA_B receptor cDNA probes were analyzed by PCR, restriction mapping and hybridization to ³²P-labeled DNA fragments representing various regions of the GABA_B receptor gene.

The cloned fragments in the plasmids pAM362, pAM363, pAM364 and pAM365 were characterized by restriction enzyme mapping, using EcoRI, HindIII, PstI, and BamHI. The approximate positions of the exons and the approximate size of the introns were analyzed and determined by PCR-based exon-exon linking and agarose gel electrophoresis.

In order to facilitate nucleotide sequence analysis, 7 restriction sub-fragments derived from pAM364, 2 restriction fragments derived from pAM362, and 1 restriction sub-fragment derived from pAM365 were isolated and cloned into pUC19, resulting in the plasmids pAM366-pAM375. The following strategy was employed; by combining PCR primers located within the pUC19 sequence either upstream or downstream of the cloning site, with a PCR primer with defined orientation and specific for the GABA_B receptor derived subcloned fragment allowed the determination.

The inserts in the 10 plasmids pAM366-pAM375 were subjected to nucleotide sequence analysis. The nucleotide sequences for all subclones were determined using a Thermo Sequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As primers for sequencing reactions specific oligonucleotides complementary to pUC19 or primers complementary to the GABA_B receptor cDNA were used.

The genomic fragments cloned in the plasmids pAM362-pAM365 were shown to contain the complete transcribed part of the human GABA_B receptor gene and extends > 3kb upstream of the first exon and > 2kb downstream of the last exon. The fragments cloned in the plasmid pAM362 were shown to contain exons 7-11, pAM363 exons 12-22, pAM364 exons 1-11, and pAM365 exons 12-23 of the GABA_B receptor gene (Figure 1). The sequence of exons 1-11 and introns 1-10 is listed in SEQ ID NO: 60 and the sequence of exons 12-23 and introns 12-22 is listed in SEQ ID NO: 61.

The human GABA_B receptor gene consists of 23 exons and 22 introns (Figure 1). The size of the exons range between 21 bp and 1486 bp. As can be noted from Table 10 exon/intron boundaries are in accordance with the AG/GT rule and conform well to the consensus sequence suggested by Mount et al. 1982.

TABLE 10

Exon-Intron boundaries of the GABA_B receptor gene, sequences at exon-intron junctions.

	5' splice donor	3' splice acceptor
Exon 1-Exon 2	CGAG	<u>GTAAGAG</u> <u>CCGCCTCTCACTTAG</u> ATGT
Exon 2-Exon 3	GAAG	<u>GTGCATC</u> <u>CGACTCACCCCTTAG</u> GTTG
Exon 3-Exon 4	TGTG	<u>GTGAGTA</u> <u>CCWATCTCTCCACAG</u> TCCG
Exon 4-Exon 5	CAGG	<u>GTGAGGG</u> <u>CTTTCCTGCTGCCAG</u> TGAA
Exon 5-Exon 6	TCAG	<u>GTGAGAT</u> <u>CGCACCCCTCCTCAG</u> AACG
Exon 6-Exon 7	CAAG	<u>GTAGCCC</u> <u>CCTCTTGCTTTTCAG</u> TGTG
Exon 7-Exon 8	TGTG	<u>GTAAGCA</u> <u>CTCCCTGCCCCACAG</u> CTTT
Exon 8-Exon 9	TTCG	<u>GTGAGGA</u> <u>TTATTCCCACCCAAG</u> ACTC
Exon 9-Exon10	GAAG	<u>GTCAGAT</u> <u>CTTTCTCTGKTGTAG</u> CGCC
Exon10-Exon11	TGAG	<u>GTGGART</u> <u>CTCCTCTGTATTCAG</u> GTGT
Exon11-Exon12	CATG	<u>GTGAGAG</u> <u>TTTTTTCCTCCCAAG</u> ACAT
Exon12-Exon13	CTCT	<u>GTGAGTT</u> <u>TGTTTCCTTCCCTCAG</u> GGCC
Exon13-Exon14	CAGG	<u>GTTAGTA</u> <u>TTGTCTGCTGCCCAG</u> GTGG
Exon14-Exon15	ATTG	<u>GTGAGTG</u> <u>CCCTGTGCCATGCAG</u> GAGG
Exon15-Exon16	TCCG	<u>GTGAGTT</u> <u>CCACCTCTGCCCTAG</u> TTAT
Exon16-Exon17	CCAG	<u>GTGAGGA</u> <u>TCTCTTCCTTCTAG</u> GCCC
Exon17-Exon18	GAAG	<u>GTGAGCT</u> <u>CACATATTTATCCAG</u> ACTC
Exon18-Exon19	TGAG	<u>GTACCAC</u> <u>TYGTTTCTGCCCTAG</u> ACAT
Exon19-Exon20	CTTG	<u>GTGTGTG</u> <u>CTCCTGCCATCCTAG</u> GCAT
Exon20-Exon21	GGCA	<u>GTGAGCA</u> <u>TGTCTTTCCCTCTAG</u> GTCC
Exon21-Exon22	CAAG	<u>GTAAGGA</u> <u>AACATTTGCCCCACAG</u> ATGC
Exon22-Exon23	TGAG	<u>GTGCGGG</u> <u>TGCTTCTTCCTCCAG</u> AAAG

5

A comparison of the sequences of the different forms of the human GABA_B receptor cDNA (SEQ ID NO: 48, 50, 54, and 56) and the sequence of the human GABA_B gene (SEQ ID NO: 60 and 61) reveals that different mRNA encoding human GABA_B receptors are formed by alternative splicing. The translational start of the GABA_B receptor 1a is localized in exon 2 and the translational stop is localized in exon 23. The mRNA encoding GABA_B receptor 1b is formed by alternative splicing where part of intron 5 is retained together with exon 6 where the translational start of the GABA_B receptor 1b is derived from the intron sequence. The mRNA encoding GABA_B receptor 1c is formed by alternative splicing where exon 15 are removed together with introns 14 and 15 and a frame shift and a translational stop are generated in the sequence corresponding to exon 16.

15

The mRNA encoding GABA_B receptor 1d is formed when the translational start of the GABA_B receptor 1b is generated together with the translational stop of the GABA_B receptor 1c.

- 5 The 1a isoform is formed by splicing exon 5 to a cryptic splice site in the middle of exon 6. Transcription of 1b isoform mRNA is most likely initiated from regulatory elements in intron 5. The ATG initiating translation of 1b mRNA is located in the 5'-end of exon 6.

10 Additional variants of the mRNA encoding variants of the human GABA_B receptor can be derived by alternative splicing where one or more of the exons or part of exons are excised in the processing of the pre-mRNA. The subsequent transcription of these mRNA will give rise to variants of the human GABA_B receptor with potentially different biological and/or pharmacological activities.

15

EXAMPLE 7. Analysis of cDNA encoding human GABA_B receptors from human brain

Messenger RNA from human fetal brain (catalog #6525-1) and adult human brain (catalog #6516-1) were obtained from Clontech (Palo Alto, CA, USA). First strand cDNA synthesis
20 reactions were performed using the first strand cDNA Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The pd(N)₆ primer was used to prime the first-strand synthesis. The generated cDNA molecules were used as templates in the PCR reactions described below.

- 25 Specific PCR primers was designed (Table 11) based on the sequences of the rat GABA_B receptor 1a and 1b cDNA and human GABA_B receptor 1a and 1b cDNA

TABLE 11

Primers used for RT-PCR on mRNA from human fetal brain

Nr	Species	Sequence 5'-3'	SEQ ID NO
838	Rat	ATGCGCGCCGGCAGCCAACATGCTGCTGCTGCTGGTGCCTCTCTTCC	62
863	Rat	GGTCATCCAGCGTTGAGGTGAAGAC	63
864	Rat	GAAGGTTGCCAGATTATACATCCGC	64
865	Rat	CCACGATGATTCGAGCATCTTGACG	65
937	Human	CTGGTTCCTCCCAATGTG	66
1015	Human	CCAGTGGACTATGAGATTGAG	67

- 5 cDNA fragments encoding parts of the human GABA_B receptors were amplified directly by PCR using the designed primers with the generated cDNA molecules as templates. PCR experiments with primers 838, 863, 864 and 865 were carried out using the Perkin Elmer Taq DNA polymerase with Gene Amp (Roche Molecular System Inc., NJ, USA) with the following PCR program: +95°C for 1 minute, +50°C for 30 seconds, +72°C for 3 minutes, repeated 44 times and finally +72°C for 7 minutes. PCR experiments with primers 937 and 1015 were carried out using the Expand Long Template PCR System (Boehringer Mannheim GmbH, Germany) with the following PCR program: +94°C for 2 minutes; +94°C for 10 seconds, +55°C for 30 seconds, +68°C for 3 minutes repeated 35 times; and finally +68°C for 7 minutes. The primer combinations 838 and 863, 864 and 863, 864 and 865, 937 and 1015 gave PCR products.

The PCR products were subcloned into the pGEM-T vector from Promega (Madison, WI, USA). The inserts were subjected to nucleotide sequence analysis. The complete nucleotide sequence for all subclones were determined using a ThermoSequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As for primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA_B receptor were used.

A number of analyzed clones isolated from fetal brain were found to lack 186 base pairs, corresponding to exon 4. This alternative splicing resulted in a cDNA (SEQ ID NO: 70)

encoding a protein (SEQ ID NO: 71) comprising of 899 amino acids and designated GABA_B receptor 1e.

Other clones from fetal brain lacked 368 base pairs, corresponding to exons 4, 5 and 6, resulting in a cDNA (SEQ ID NO: 72) where a frame shift and a translational stop codon are generated in the sequence corresponding to exon 7, encoding a protein (SEQ ID NO: 73) comprising only 97 amino acids designated GABA_B receptor 1f.

One clone lacked 207 base pairs, corresponding to exons 4 and 5, resulting in a cDNA (SEQ ID NO: 74) encoding a protein (SEQ ID NO: 75) comprising 892 amino acids designated GABA_B receptor 1g.

Another clone had two deletions, the first comprising 186 base pairs corresponding to exon 4, the second comprising 39 base pairs corresponding to part of exon 6, resulting in a cDNA (SEQ ID NO: 76) encoding a protein (SEQ ID NO: 77) comprising 886 amino acids designated GABA_B receptor 1h.

Yet another clone from adult human brain was found to have a long deletion comprising 1194 base pairs corresponding to base pairs 319 - 1512 of the cDNA encoding human GABA_B receptor 1a. This deletion corresponds to part of exon 4, exons 5-11, and part of exon 12. This cDNA (SEQ ID NO: 78) encodes a protein (SEQ ID NO: 79) comprising 563 amino acids designated GABA_B receptor 1i.

One clone isolated from fetal brain lacked 284 base pairs corresponding to part of exon 3 and the whole exon 4, generating a frame shift and a translational stop codon in the sequence corresponding to exon 5. This cDNA (SEQ ID NO: 80) encodes a protein (SEQ ID NO: 81) comprising only 105 amino acids designated GABA_B receptor 1j.

EXAMPLE 8. Analysis of cDNA encoding human GABA_B receptors from Jurkat cells

A guanidinisothiocyanate/CsCl method was used to isolate total RNA from Jurkat cells. First strand cDNA synthesis reactions were performed using the first strand cDNA

Synthesis kit from Amersham Pharmacia Biotech (Uppsala, Sweden). The pd(N)₆ primer was used to prime the first-strand synthesis. The generated cDNA molecules were used as templates in the PCR reactions described below.

- 5 Specific PCR primers was designed (Table 12) based on the sequences of the human GABA_B receptor 1a and 1b cDNA

TABLE 12

Primers used for RT-PCR on mRNA from Jurkat cells

10

Nr	Species	Sequence 5'-3'	SEQ ID NO
937	Human	CTGGTTCCTCCCAATGTG	68
1015	Human	CCAGTGGACTATGAGATTGAG	69

- cDNA fragments encoding parts of the human GABA_B receptors were amplified directly by PCR using the designed primers with the generated cDNA molecules as templates. The PCR experiment was carried out using the Expand Long Template PCR System (Boehringer Mannheim GmbH, Germany) with the following PCR program: +94°C for 2 minutes; +94°C for 10 seconds, +55°C for 30 seconds, +68°C for 3 minutes repeated 35 times; and finally +68°C for 7 minutes. The primer combination 937 and 1015 gave a PCR product.

- 20 The PCR products were subcloned into the pGEM-T vector from Promega (Madison, WI, USA). The inserts were subjected to nucleotide sequence analysis. The complete nucleotide sequence for all subclones were determined using a ThermoSequenase dye terminator cycle sequencing pre-mix kit (Amersham Pharmacia Biotech, Uppsala, Sweden). As for primers for sequencing reactions specific oligonucleotides complementary to the vector pGEM-T or primers complementary to the cDNA encoding the GABA_B receptor were used.

- Two clones had two deletions, the first comprising 368 base pairs corresponding to exons 4, 5 and 6, the second comprising 151 base pairs corresponding to exon 15 where a frame shift and a translational stop codon are generated in the sequence corresponding to exon 7.
- 30 This cDNA (SEQ ID NO: 82) encodes a protein (SEQ ID NO: 83) comprising only 98

amino acids designated GABA_B receptor 1k which is identical to the GABA_B receptor 1f described above.

Another two clones also had two deletions, the first comprising 246 base pairs corresponding to part of exon 4, exon 5 and exon 6, the second comprising 149 base pairs corresponding to exon 15, generating a frame shift and a translational stop codon in the sequence corresponding to exon 16. This cDNA (SEQ ID NO: 84) encodes a protein (SEQ ID NO: 5) comprising 496 amino acids designated GABA_B receptor 1l.

- 10 Additional variants of cDNA encoding the human GABA_B receptors can be identified in a similar manner using PCR primers based on the sequence of the cDNA and genomic fragments encoding the human GABA_B receptors disclosed in the present application.

- 15 The biological activity of these variants of the human GABA_B receptor can be evaluated by transfection of suitable host cells with expression vectors comprising the corresponding cDNA sequences and subsequent measurement of binding of labeled ligands or activation of the receptor or modulation of receptor function.

20 EXAMPLE 9: Generation of antibodies

- Antibodies were raised in rabbits against four different BSA-conjugated 20 amino acids long synthetic peptides corresponding to selected regions of the human and canine GABA_B receptor extracellular domain. Two were directed against a sequence common for GABA_B receptor 1a and b (ab1 and ab2), one against a GABA_B receptor 1a-specific region (a1) and one against a GABA_B receptor 1b-specific sequence (b1). To allow BSA-conjugation, a cystein residue was added to the N-terminus in all peptides but a1, which contains an endogenous cystein.

- 30 Peptide a1: (SEQ ID NO: 49 amino acids 18-37)

Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile Ile His Pro Pro Trp

Peptide ab1: (SEQ ID NO: 49 amino acids 197-216 with N-terminally added Cys)

Cys - Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu Ile
His His

5 Peptide ab2: (SEQ ID NO: 49 amino acids 271-290 with N-terminally added Cys)

Cys - Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro
Ser Ala

Peptide b1: (SEQ ID NO: 57 amino acids 30-47 with N-terminally added Cys)

10 Cys - Ser His Ser Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser

The antibodies were purified from rabbit serum by affinity chromatography using the
corresponding immobilized peptide and subsequently used to detect expression of
recombinant GABA_B receptor isoforms on Western blots.

15

EXAMPLE 10: Heterologous expression of GABA_B receptor isoforms in mammalian cells

A HindIII / SalI cDNA fragment encoding the human GABA_B receptor 1b isoform was
20 cloned into a BPV (bovine papilloma virus)-based expression vector containing the mMT-
1 (murine metallothioneine) promoter. Using the calcium phosphate method, murine C127
cells were co-transfected with the GABA_B receptor expression construct and an expression
plasmid containing a G418 resistance marker gene using the calcium phosphate method.
G418 resistant clones were evaluated by Western blot analysis for expression of the
25 approximately 100 kDa GABA_B receptor 1b isoform(Figure 2). Similarly, but using
Lipofectamine (Life Technologies Inc, Rockville, MD, USA) for transfection, the human
GABA_B receptor 1b isoform was expressed in human HEK-293 cells using the pCI-neo
expression vector. The identity of the heterologously expressed receptor was verified in
HEK-293 cells by Western blot analysis and radioligand binding experiments.

30

A cDNA fragment encoding the human GABA_B receptor 1d isoform was cloned into a
BPV-based expression vector containing the mMT-1 promoter. Using the calcium
phosphate method, murine C127 cells were co-transfected with the GABA_B receptor

expression construct and an expression plasmid containing a G418 resistance marker gene. G418 resistant clones, and concentrated medium from the same clones, were evaluated for GABA_B receptor 1d isoform expression by Western blot analysis (Figure 3). The experiment revealed the human GABA_B receptor 1d to be a secreted isoform.

5

EXAMPLE 11: Heterologous expression of GABA_B receptor isoforms in *E. coli*

A cDNA fragment encoding the human GABA_B receptor 1d isoform was cloned into a modified pET (Pharmacia Amersham, Uppsala, Sweden) vector downstream of a STII (heat stable enterotoxin II of *E. coli*) signal peptide and followed by a thrombin cleavage site and a hexahistidine tag. The expression construct was subsequently used to transform the BL21 (DE3) *E. coli* strain. Western blot analysis of IPTG-induced bacteria revealed expression of a human GABA_B receptor 1d isoform of expected size (Figure 4).

15

In addition, the human GABA_B receptor 1d isoform was successfully expressed without fusion to a bacterial signal peptide in *E. coli* strain AD494 (DE3).

EXAMPLE 12: Method for the screening of substances which are GABA_B receptor antagonists or agonists

GABA_B receptor expressing cells, transgenic animals or cells and tissues derived thereof, are used to screen substance libraries for antagonist or agonist activities. Screening is performed as ligand binding assays or functional assays. For screening, cells and tissues are prepared in various ways, each uniquely suited to its purpose. Ligand binding assays are performed *in vivo* or *in vitro*. Functional assays exemplified by, but not limited to, Ca⁺⁺-responses, cAMP-responses and effects on Cl⁻ and K⁺ channels, are performed in living cells, broken cells, isolated cell membranes, as well as in tissues and in living animals.

25

CLAIMS

1. A nucleic acid molecule encoding a human or canine GABA_B receptor, or a functionally equivalent modified form thereof.
- 5 2. A nucleic acid molecule according to claim 1 encoding a human GABA_B receptor, or a functionally equivalent modified form thereof.
3. A nucleic acid molecule according to claim 2 encoding the human GABA_B receptor
10 1a, or a functionally equivalent modified form thereof.
4. A nucleic acid molecule according to claim 3 selected from:
(a) a nucleic acid molecule comprising a nucleotide sequence set forth as SEQ ID NO: 48;
15 (b) a nucleic acid molecule comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary to the polypeptide coding region of a DNA molecule as defined in (a); and
(c) a nucleic acid molecule comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleotide sequence as defined in (a) or (b).
- 20 5. A nucleic acid molecule according to claim 2 encoding the human GABA_B receptor 1b, or a functionally equivalent modified form thereof..
6. A nucleic acid molecule according to claim 5 selected from:
25 (a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 50;
(b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary the polypeptide coding region of a DNA molecule as defined in (a); and
30 (c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleotide sequence as defined in (a) or (b).

7. A nucleic acid molecule according to claim 2 encoding the human GABA_B receptor 1c, or a functionally equivalent modified form thereof.
8. A nucleic acid molecule according to claim 7 selected from:
- 5 (a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 54;
- (b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary the polypeptide coding region of a DNA molecule as defined in (a); and
- 10 (c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleotide sequence as defined in (a) or (b).
9. A nucleic acid molecule according to claim 2 encoding the human GABA_B receptor 1d, or a functionally equivalent modified form thereof..
- 15 10. A nucleic acid molecule according to claim 9 selected from:
- (a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 56;
- (b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing,
- 20 under stringent hybridization conditions, to a nucleotide sequence complementary the polypeptide coding region of a DNA molecule as defined in (a); and
- (c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleotide sequence as defined in (a) or (b).
- 25 11. A nucleic acid molecule according to claim 1 encoding a canine GABA_B receptor, or a functionally equivalent modified form thereof.
12. A nucleic acid molecule according to claim 11 encoding the canine GABA_B receptor 1a, or a functionally equivalent modified form thereof.
- 30 13. A nucleic acid molecule according to claim 12 selected from

(a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 52;

(b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary the polypeptide coding region of a DNA molecule as defined in (a); and

(c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleic acid sequence as defined in (a) or (b).

14 A nucleic acid molecule according to claim 11 encoding the canine GABA_B receptor 1c, or a functionally equivalent modified form thereof.

15 A nucleic acid molecule according to claim 14 selected from

(a) nucleic acid molecules comprising a nucleotide sequence set forth as SEQ ID NO: 58;

(b) nucleic acid molecules comprising a nucleotide sequence capable of hybridizing, under stringent hybridization conditions, to a nucleotide sequence complementary the polypeptide coding region of a DNA molecule as defined in (a); and

(c) nucleic acid molecules comprising a nucleotide sequence which is degenerate as a result of the genetic code to a nucleic acid sequence as defined in (a) or (b).

16 A recombinant polypeptide encoded by a nucleotide sequence according to any one of claims 1 to 15.

17 The polypeptide according to claim 16 comprising an amino acid sequence set forth as SEQ ID NO: 49, 51, 53, 55, 57 or 59 in the Sequence Listing.

18 A polypeptide according to claim 16 which has been posttranslationally modified.

19 A vector transformed with a nucleic acid molecule according to any one of claims 1 to 15.

20 A cultured host cell harboring a vector according to claim 19.

21. A process for the production of a GABA_B receptor, said process comprising culturing a host cell according to claim 20 under conditions whereby the said polypeptide is produced, and recovering the said polypeptide.
- 5 22. A method for the screening of compounds which are inhibitors of transient lower esophageal sphincter relaxations, said method comprising the use of a nucleic acid molecule encoding a GABA_B receptor.
- 10 23. A method according to claim 22 wherein the said nucleic acid molecule encoding a GABA_B receptor is the nucleic acid molecule according to any one of claims 1 to 15.
24. A method for the screening of compounds which are agonists or antagonists to a GABA_B receptor, said method comprising the use of a nucleic acid molecule
15 according to any one of claims 1 to 15.
25. A method according to any one of claims 22 to 24 comprising the steps (a) transforming a cultured cell with a nucleic acid molecule encoding a GABA_B receptor, so that a GABA_B receptor is expressed on the surface of the cell; (b)
20 contacting a test compound with the said cell; and (c) determining whether the test compound binds to, and/or activate, the GABA_B receptor.
26. A pharmaceutical compositions comprising a soluble GABA_B receptor further comprising one or more pharmaceutical acceptable carriers and/or diluents.

1/2

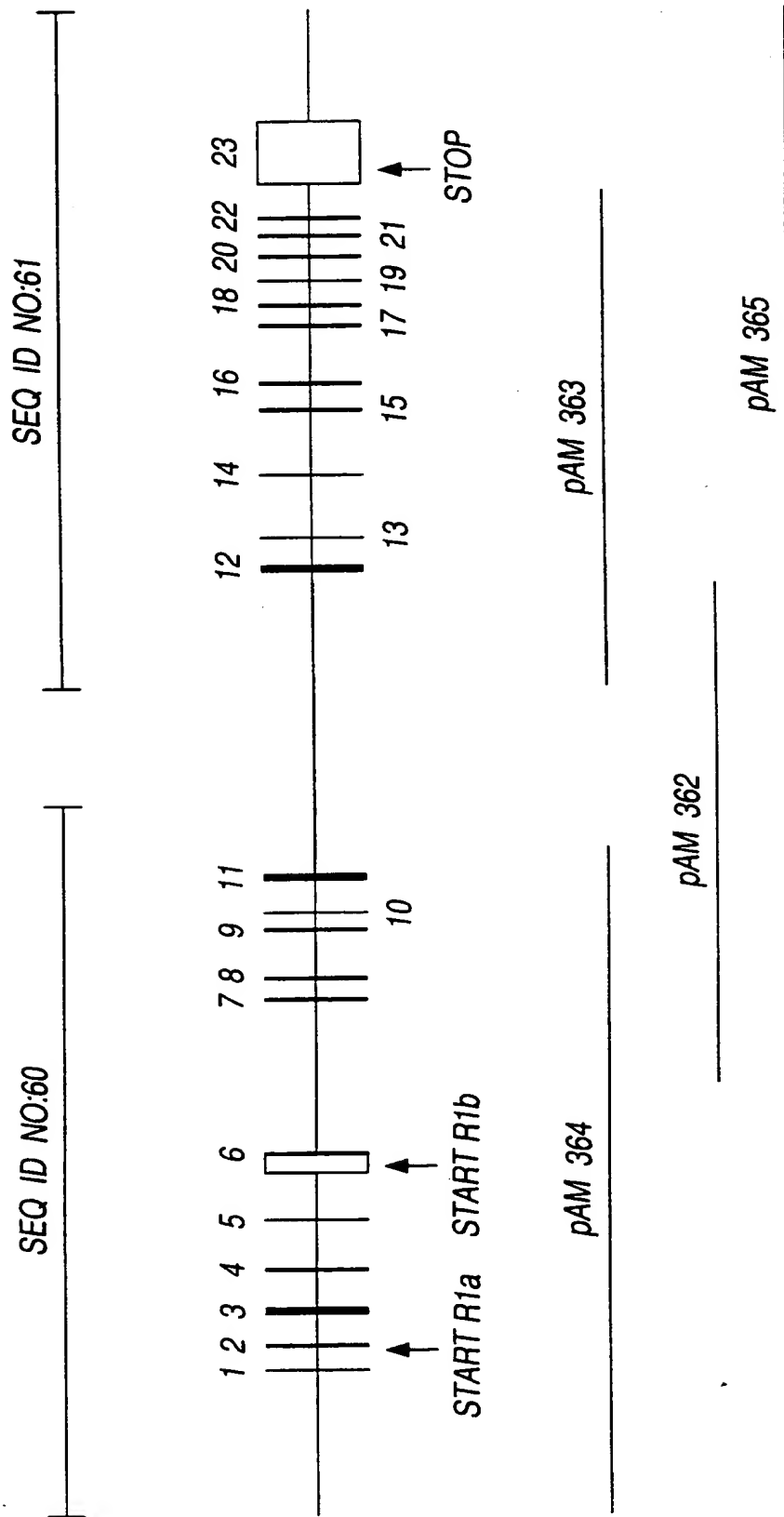


Fig.1

2/2

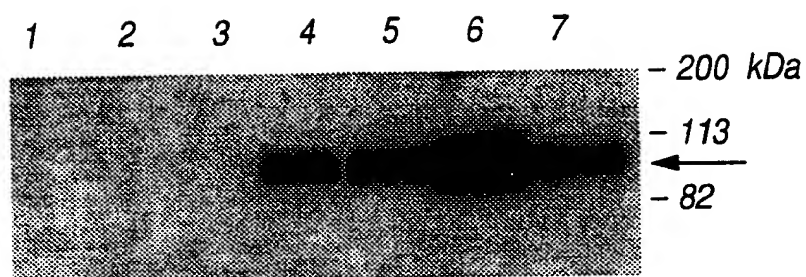


Fig.2

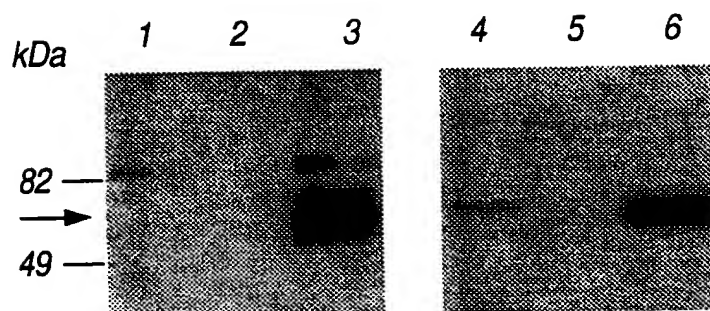


Fig.3

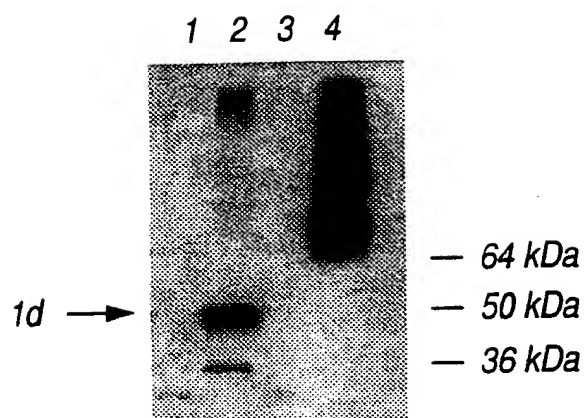


Fig.4

SEQUENCE LISTING

5

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: ASTRA AB
10 (B) STREET: Västra Mälarehamnen 9
(C) CITY: Södertälje
(E) COUNTRY: Sweden
(F) POSTAL CODE (ZIP): S-151 85
(G) TELEPHONE: +46-8-553 260 00
15 (H) TELEFAX: +46-8-553 288 20
(I) TELEX: 19237 astra s

(ii) TITLE OF INVENTION: New nucleotide sequences

20 (iii) NUMBER OF SEQUENCES: 85

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

40

GTTTCTTCTC GGATCCAGCT GTGCCTG

27

(2) INFORMATION FOR SEQ ID NO: 2:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

15 CAGGCACAGC TGGATCCGAG AAGAAACT

28

(2) INFORMATION FOR SEQ ID NO: 3:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

30 CGGTCGACTC ACTTGTAAG CAAATGTACT CGACTCCC

38

(2) INFORMATION FOR SEQ ID NO: 4:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATGCGCGCCG GCAGCCAACA TGCTGCTGCT GCTGCTGGTG C

41

5 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CGGTGCTCTC ACTTGTAAG CAAATGTACT CGACTCCCAT CACAGC

46

20 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

ATGCGCGCCG GCAGCCAACA TGCTGCTGCT GCTGCTGGTG CCTCTCTTCC

50

35 (2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGGCACAGC TGGATCCGAG AAGAAACTCT GTCGGAAAGT

40

5

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGTCATCCAG CGTTGAGGTG AAGAC

25

20

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GAAGGTTGCC AGATTATACA TCCGC

25

35

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

5

CCACGATGAT TCGAGCATCT TGACG

25

(2) INFORMATION FOR SEQ ID NO: 11:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

20

GCCTCTCACT CCCCTCATCT CC

22

(2) INFORMATION FOR SEQ ID NO: 12:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

35

GAGTGAAGGA GGCTGGAATT G

21

(2) INFORMATION FOR SEQ ID NO: 13:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GACGCTTATC GAGCAGCTTC

20

10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AGCCCAGAAC TCACAGGGGG ACAT

24

25

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GCTTCAAGCC AGGTACGAAC TAA

23

40

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

10

TGGCCCTCCA CCGCCTCAGT CATCTCA

27

(2) INFORMATION FOR SEQ ID NO: 17:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

25

CCATCCTAAT ACGACTCACT ATAGGGC

27

(2) INFORMATION FOR SEQ ID NO: 18:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

40

CTCAATCTCA TAGTCCACTG G

21

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CCTTGAGGCC CGGGGAGAG

19

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CAGGCACAGC TGGATCCGAG AAGAAACT

28

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CGGTCGACTC ACTTGTAAG CAAATGTACT CGACTCCCAT CACAGC

46

(2) INFORMATION FOR SEQ ID NO: 22:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

15 ATGCGCGCCG GCAGCCAACA TGCTGCTGCT GCTGCTGGTG CCTCTCTTCC

50

(2) INFORMATION FOR SEQ ID NO: 23:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

30 CGTCAAGATG CTCGAATCAT CG

22

(2) INFORMATION FOR SEQ ID NO: 24:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CAGGGGGCTC AGAGGGTCCC

20

5 (2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CAGGCACAGC TGGATCCGAG AAGAACTCT GTCGGAAAGT

40

20 (2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CGGTCGACTC ACTTGTAAG CAAATGTACT CGACTCCCAT CACAGCTAAG

50

35 (2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ACTTTCGAC AGAGTTTCTT CTCGGATCCA GCTGTGCCTG

40

5

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CCACGATGAT TCGAGCATCT TGACG

25

20

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CTACCGCGCA ATGAACTCCT CGTC

24

35

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

5

CGAGGTGGCG TTGGGGGTCT GTGC

24

(2) INFORMATION FOR SEQ ID NO: 31:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

20

CCATCCTAAT ACGACTCACT ATAGGGC

27

(2) INFORMATION FOR SEQ ID NO: 32:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

35

ACTCACTATA GGGCTCGAGC GGC

23

(2) INFORMATION FOR SEQ ID NO: 33:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GACGCTTATC GAGCAGCTTC

20

10

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AGCCCAGAAC TCACAGGGGG ACAT

24

25

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GCTTCAAGCC AGGTACGAAC TAA

23

40

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

10 GGAGCACCCC CAAGCCCCAC TG

22

(2) INFORMATION FOR SEQ ID NO: 37:

- 15 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

25 CTGGTTCCTC CCAATGTG

18

(2) INFORMATION FOR SEQ ID NO: 38:

- 30 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

40 CCTCTCACTC CCCTCATCTC

20

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

AAGCCAACCT TCCCTGCTTC TC

22

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CTGGTTCCTC CCAATGTG

18

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GACGCTTATC GAGCAGCTTC

20

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

15 CTACCGCGCA ATGAACTCCT CGTC

24

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

30 CCTTCTTCTC CTCCTTCTTA GTGA

24

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 2883 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

5

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..2883

10

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Kaupmann, K

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15

Bischoff, S

Mickel, S

McMaster, G

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Bittiger, H

20

Froestl, W

(B) TITLE: Expression cloning of GABA-B receptors
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receptors

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25

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(F) PAGES: 239-246

(G) DATE: 20 march-1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

30

ATG CTG CTG CTG CTG CTG GTG CCT CTC TTC CTC CGC CCC CTG GGC GCT	48
Met Leu Leu Leu Leu Leu Val Pro Leu Phe Leu Arg Pro Leu Gly Ala	
1 5 10 15	

35

GGC GGG GCG CAG ACC CCC AAC GCC ACC TCG GAA GGT TGC CAG ATT ATA	96
Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile Ile	
20 25 30	

40

CAT CCG CCC TGG GAA GGT GGC ATC AGG TAC CGT GGC TTG ACT CGC GAC	144
His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg Asp	
35 40 45	

CAG GTG AAG GCC ATC AAC TTC CTG CCT GTG GAC TAT GAG ATC GAA TAT	192
---	-----

	Gln	Val	Lys	Ala	Ile	Asn	Phe	Leu	Pro	Val	Asp	Tyr	Glu	Ile	Glu	Tyr	
	50						55					60					
	GTG	TGC	CGA	GGG	GAG	CGC	GAG	GTG	GTG	GGG	CCC	AAG	GTG	CGC	AAA	TGC	240
5	Val	Cys	Arg	Gly	Glu	Arg	Glu	Val	Val	Gly	Pro	Lys	Val	Arg	Lys	Cys	
	65					70				75					80		
	CTG	GCC	AAC	GGC	TCC	TGG	ACG	GAT	ATG	GAC	ACA	CCC	AGC	CGC	TGT	GTC	288
10	Leu	Ala	Asn	Gly	Ser	Trp	Thr	Asp	Met	Asp	Thr	Pro	Ser	Arg	Cys	Val	
				85					90					95			
	CGA	ATC	TGC	TCC	AAG	TCT	TAT	TTG	ACC	CTG	GAA	AAT	GGG	AAG	GTT	TTC	336
	Arg	Ile	Cys	Ser	Lys	Ser	Tyr	Leu	Thr	Leu	Glu	Asn	Gly	Lys	Val	Phe	
				100					105					110			
15	CTG	ACG	GGT	GGG	GAC	CTC	CCA	GCT	CTG	GAT	GGA	GCC	CGG	GTG	GAG	TTC	384
	Leu	Thr	Gly	Gly	Asp	Leu	Pro	Ala	Leu	Asp	Gly	Ala	Arg	Val	Glu	Phe	
				115					120					125			
20	CGA	TGT	GAC	CCC	GAC	TTC	CAT	CTG	GTG	GGC	AGC	TCC	CGG	AGC	GTC	TGT	432
	Arg	Cys	Asp	Pro	Asp	Phe	His	Leu	Val	Gly	Ser	Ser	Arg	Ser	Val	Cys	
		130					135					140					
	AGT	CAG	GGC	CAG	TGG	AGC	ACC	CCC	AAG	CCC	CAC	TGC	CAG	GTG	AAT	CGA	480
25	Ser	Gln	Gly	Gln	Trp	Ser	Thr	Pro	Lys	Pro	His	Cys	Gln	Val	Asn	Arg	
	145					150					155				160		
	ACG	CCA	CAC	TCA	GAA	CGG	CGT	GCA	GTA	TAC	ATC	GGG	GCG	CTG	TTT	CCC	528
30	Thr	Pro	His	Ser	Glu	Arg	Arg	Ala	Val	Tyr	Ile	Gly	Ala	Leu	Phe	Pro	
				165						170				175			
	ATG	AGC	GGG	GGC	TGG	CCG	GGG	GGC	CAG	GCC	TGC	CAG	CCC	GCG	GTG	GAG	576
	Met	Ser	Gly	Gly	Trp	Pro	Gly	Gly	Gln	Ala	Cys	Gln	Pro	Ala	Val	Glu	
				180					185					190			
35	ATG	GCG	CTG	GAG	GAC	GTT	AAC	AGC	CGC	AGA	GAC	ATC	CTG	CCG	GAC	TAC	624
	Met	Ala	Leu	Glu	Asp	Val	Asn	Ser	Arg	Arg	Asp	Ile	Leu	Pro	Asp	Tyr	
				195					200					205			
40	GAG	CTC	AAG	CTT	ATC	CAC	CAC	GAC	AGC	AAG	TGT	GAC	CCA	GGG	CAA	GCC	672
	Glu	Leu	Lys	Leu	Ile	His	His	Asp	Ser	Lys	Cys	Asp	Pro	Gly	Gln	Ala	
		210						215						220			

	ACC AAG TAC TTG TAC GAA CTA CTC TAC AAT GAC CCC ATC AAG ATC ATT	720
	Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile	
	225 230 235 240	
5	CTC ATG CCT GGC TGT AGT TCT GTC TCC ACA CTT GTA GCT GAG GCT GCC	768
	Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala	
	245 250 255	
10	CGG ATG TGG AAC CTT ATT GTG CTC TCA TAT GGC TCC AGT TCA CCA GCC	816
	Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala	
	260 265 270	
15	TTG TCA AAC CGA CAG CGG TTT CCC ACG TTC TTC CGG ACG CAT CCA TCC	864
	Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser	
	275 280 285	
20	GCC ACA CTC CAC AAT CCC ACC CGG GTG AAA CTC TTC GAA AAG TGG GGC	912
	Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly	
	290 295 300	
25	TGG AAG AAG ATC GCT ACC ATC CAA CAG ACC ACC GAG GTC TTC ACC TCA	960
	Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser	
	305 310 315 320	
30	ACG CTG GAT GAC CTG GAG GAG CGA GTG AAA GAG GCT GGG ATC GAG ATC	1008
	Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile	
	325 330 335	
35	ACT TTC CGA CAG AGT TTC TTC TCG GAT CCA GCT GTG CCT GTT AAA AAC	1056
	Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn	
	340 345 350	
40	CTG AAG CGT CAA GAT GCT CGA ATC ATC GTG GGA CTT TTC TAT GAG ACG	1104
	Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr	
	355 360 365	
45	GAA GCC CGG AAA GTT TTT TGT GAG GTC TAT AAG GAA AGG CTC TTT GGG	1152
	Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly	
	370 375 380	
50	AAG AAG TAC GTC TGG TTC CTC ATC GGG TGG TAT GCT GAC AAC TGG TTC	1200
	Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe	
	385 390 395 400	

	AAG ACC TAT GAC CCG TCA ATC AAT TGT ACA GTG GAA GAA ATG ACC GAG	1248
	Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Glu Glu Met Thr Glu	
	405 410 415	
5	GCG GTG GAG GGC CAC ATC ACC ACG GAG ATT GTC ATG CTG AAC CCT GCC	1296
	Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala	
	420 425 430	
10	AAC ACC CGA AGC ATT TCC AAC ATG ACG TCA CAG GAA TTT GTG GAG AAA	1344
	Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys	
	435 440 445	
15	CTA ACC AAG CGG CTG AAA AGA CAC CCC GAG GAG ACT GGA GGC TTC CAG	1392
	Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln	
	450 455 460	
20	GAG GCA CCA CTG GCC TAT GAT GCT ATC TGG GCC TTG GCT TTG GCC TTG	1440
	Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu	
	465 470 475 480	
25	AAC AAG ACG TCT GGA GGA GGT GGT CGT TCC GGC GTG CGC CTG GAG GAC	1488
	Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp	
	485 490 495	
30	TTT AAC TAC AAC AAC CAG ACC ATT ACA GAC CAG ATC TAC CGG GCC ATG	1536
	Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met	
	500 505 510	
35	AAC TCC TCC TCC TTT GAG GGC GTT TCT GGC CAT GTG GTC TTT GAT GCC	1584
	Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala	
	515 520 525	
40	AGC GGC TCC CGG ATG GCA TGG ACA CTT ATC GAG CAG CTA CAG GGC GGC	1632
	Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly	
	530 535 540	
45	AGC TAC AAG AAG ATC GGC TAC TAC GAC AGC ACC AAG GAT GAT CTT TCC	1680
	Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser	
	545 550 555 560	
50	TGG TCC AAA ACG GAC AAG TGG ATT GGA GGG TCT CCC CCA GCT GAC CAG	1728
	Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln	

	565	570	575	
	ACC TTG GTC ATC AAG ACA TTC CGT TTC CTG TCT CAG AAA CTC TTT ATC			1776
	Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile			
5	580	585	590	
	TCC GTC TCA GTT CTC TCC AGC CTG GGC ATT GTT CTT GCT GTT GTC TGT			1824
	Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys			
	595	600	605	
10	CTG TCC TTT AAC ATC TAC AAC TCC CAC GTT CGT TAT ATC CAG AAC TCC			1872
	Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser			
	610	615	620	
15	CAG CCC AAC CTG AAC AAT CTG ACT GCT GTG GGC TGC TCA CTG GCA CTG			1920
	Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu			
	625	630	635	640
	GCT GCT GTC TTC CCT CTC GGG CTG GAT GGT TAC CAC ATA GGG AGA AGC			1968
20	Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Ser			
	645	650	655	
	CAG TTC CCG TTT GTC TGC CAG GCC CGC CTT TGG CTC TTG GGC TTG GGC			2016
	Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly			
25	660	665	670	
	TTT AGT CTG GGC TAT GGC TCT ATG TTC ACC AAG ATC TGG TGG GTC CAC			2064
	Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His			
	675	680	685	
30	ACA GTC TTC ACG AAG AAG GAG GAG AAG AAG GAG TGG AGG AAG ACC CTA			2112
	Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu			
	690	695	700	
35	GAG CCC TGG AAA CTC TAT GCC ACT GTG GGC CTG CTG GTG GGC ATG GAT			2160
	Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp			
	705	710	715	720
	GTC CTG ACT CTT GCC ATC TGG CAG ATT GTG GAC CCC TTG CAC CGA ACC			2208
40	Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr			
	725	730	735	
	ATT GAG ACT TTT GCC AAG GAG GAA CCA AAG GAA GAC ATC GAT GTC TCC			2256

	Ile	Glu	Thr	Phe	Ala	Lys	Glu	Glu	Pro	Lys	Glu	Asp	Ile	Asp	Val	Ser	
					740				745						750		
	ATT	CTG	CCC	CAG	TTG	GAG	CAC	TGC	AGC	TCC	AAG	AAG	ATG	AAT	ACG	TGG	2304
5	Ile	Leu	Pro	Gln	Leu	Glu	His	Cys	Ser	Ser	Lys	Lys	Met	Asn	Thr	Trp	
			755					760					765				
	CTT	GGC	ATT	TTC	TAT	GGT	TAC	AAG	GGG	CTG	CTG	CTG	CTG	CTG	GGA	ATC	2352
10	Leu	Gly	Ile	Phe	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	Leu	Leu	Gly	Ile	
		770					775						780				
	TTT	CTT	GCT	TAC	GAA	ACC	AAG	AGC	GTG	TCC	ACT	GAA	AAG	ATC	AAT	GAC	2400
	Phe	Leu	Ala	Tyr	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	Lys	Ile	Asn	Asp	
	785					790					795				800		
15	CAC	AGG	GCC	GTG	GGC	ATG	GCT	ATC	TAC	AAT	GTC	GCG	GTC	CTG	TGT	CTC	2448
	His	Arg	Ala	Val	Gly	Met	Ala	Ile	Tyr	Asn	Val	Ala	Val	Leu	Cys	Leu	
				805					810					815			
20	ATC	ACT	GCT	CCT	GTG	ACC	ATG	ATC	CTT	TCC	AGT	CAG	CAG	GAC	GCA	GCC	2496
	Ile	Thr	Ala	Pro	Val	Thr	Met	Ile	Leu	Ser	Ser	Gln	Gln	Asp	Ala	Ala	
				820					825					830			
	TTT	GCC	TTT	GCC	TCT	CTG	GCC	ATC	GTG	TTC	TCT	TCC	TAC	ATC	ACT	CTG	2544
25	Phe	Ala	Phe	Ala	Ser	Leu	Ala	Ile	Val	Phe	Ser	Ser	Tyr	Ile	Thr	Leu	
			835					840					845				
	GTT	GTG	CTC	TTT	GTG	CCC	AAG	ATG	CGC	AGG	CTG	ATC	ACC	CGA	GGG	GAA	2592
30	Val	Val	Leu	Phe	Val	Pro	Lys	Met	Arg	Arg	Leu	Ile	Thr	Arg	Gly	Glu	
		850					855					860					
	TGG	CAG	TCT	GAA	ACG	CAG	GAC	ACC	ATG	AAA	ACA	GGA	TCA	TCC	ACC	AAC	2640
	Trp	Gln	Ser	Glu	Thr	Gln	Asp	Thr	Met	Lys	Thr	Gly	Ser	Ser	Thr	Asn	
	865					870					875				880		
35	AAC	AAC	GAG	GAA	GAG	AAG	TCC	CGA	CTG	TTG	GAG	AAG	GAA	AAC	CGA	GAA	2688
	Asn	Asn	Glu	Glu	Glu	Lys	Ser	Arg	Leu	Leu	Glu	Lys	Glu	Asn	Arg	Glu	
				885					890					895			
40	CTG	GAA	AAG	ATC	ATC	GCT	GAG	AAA	GAG	GAG	CGC	GTC	TCT	GAA	CTG	CGC	2736
	Leu	Glu	Lys	Ile	Ile	Ala	Glu	Lys	Glu	Glu	Arg	Val	Ser	Glu	Leu	Arg	
				900					905					910			

CAT CAG CTC CAG TCT CGG CAG CAA CTC CGC TCA CGG CGC CAC CCC CCA 2784
 His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro
 915 920 925

5 ACA CCC CCA GAT CCC TCT GGG GGC CTT CCC AGG GGA CCC TCT GAG CCC 2832
 Thr Pro Pro Asp Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro
 930 935 940

CCT GAC CGG CTT AGC TGT GAT GGG AGT CGA GTA CAT TTG CTT TAC AAG 2880
 10 Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys
 945 950 955 960

TGA 2883
 *

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(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 960 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Met Leu Leu Leu Leu Leu Val Pro Leu Phe Leu Arg Pro Leu Gly Ala
 1 5 10 15

30 Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile Ile
 20 25 30

His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg Asp
 35 35 40 45

Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu Tyr
 50 55 60

40 Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys Cys
 65 70 75 80

Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys Val

	85	90	95
	Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val Phe		
	100	105	110
5	Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Glu Phe		
	115	120	125
	Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Val Cys		
10	130	135	140
	Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn Arg		
	145	150	155
15	Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro		
	165	170	175
	Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu		
	180	185	190
20	Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr		
	195	200	205
	Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala		
25	210	215	220
	Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile		
	225	230	235
30	Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala		
	245	250	255
	Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala		
	260	265	270
35	Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser		
	275	280	285
	Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly		
40	290	295	300
	Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser		
	305	310	315
			320

Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile
 325 330 335

5 Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn
 340 345 350

Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr
 355 360 365

10 Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly
 370 375 380

Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe
 15 385 390 395 400

Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Glu Glu Met Thr Glu
 405 410 415

20 Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala
 420 425 430

Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys
 435 440 445

25 Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln
 450 455 460

Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu
 30 465 470 475 480

Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp
 485 490 495

35 Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met
 500 505 510

Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala
 515 520 525

40 Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly
 530 535 540

Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser
 545 550 555 560

Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln
 5 565 570 575

Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile
 580 585 590

10 Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys
 595 600 605

Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser
 610 615 620

15 Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu
 625 630 635 640

Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Ser
 20 645 650 655

Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly
 660 665 670

25 Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His
 675 680 685

Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu
 690 695 700

30 Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp
 705 710 715 720

Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr
 35 725 730 735

Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser
 740 745 750

40 Ile Leu Pro Gln Leu Glu His Cys Ser Ser Lys Lys Met Asn Thr Trp
 755 760 765

Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly Ile

	770	775	780
	Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp		
	785	790	795 800
5	His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu		
	805	810	815
	Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala		
10	820	825	830
	Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu		
	835	840	845
15	Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu		
	850	855	860
	Trp Gln Ser Glu Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn		
	865	870	875 880
20	Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu		
	885	890	895
	Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg		
25	900	905	910
	His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro		
	915	920	925
30	Thr Pro Pro Asp Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro		
	930	935	940
	Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys		
	945	950	955 960

35

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 2538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

5

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

10

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..2532

15

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Kaupmann, K

Huggel, K

Heid, J

Flor, P

20

Bischoff, M

Mickel, S

McMaster, G

Angst, C

Bittiger, H

25

Froestl, W

(B) TITLE: Expression cloning of GABA-B receptors

uncovers similarity to metabotropic glutamate
receptors

(C) JOURNAL: Nature

30

(D) VOLUME: 386

(F) PAGES: 239-246

(G) DATE: 20 March-1997

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

ATG GGC CCG GGG GGA CCC TGT ACC CCA GTG GGG TGG CCG CTG CCT CTT 48
Met Gly Pro Gly Gly Pro Cys Thr Pro Val Gly Trp Pro Leu Pro Leu
1 5 10 15

40

CTG CTG GTG ATG GCG GCT GGG GTG GCT CCG GTG TGG GCC TCT CAC TCC 96
Leu Leu Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser
20 25 30

	CCT CAT CTC CCG CGG CCT CAC CCG AGG GTC CCC CCG CAC CCC TCC TCA	144
	Pro His Leu Pro Arg Pro His Pro Arg Val Pro Pro His Pro Ser Ser	
	35 40 45	
5	GAA CGG CGT GCA GTA TAC ATC GGG GCG CTG TTT CCC ATG AGC GGG GGC	192
	Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly	
	50 55 60	
10	TGG CCG GGG GGC CAG GCC TGC CAG CCC GCG GTG GAG ATG GCG CTG GAG	240
	Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu	
	65 70 75 80	
15	GAC GTT AAC AGC CGC AGA GAC ATC CTG CCG GAC TAC GAG CTC AAG CTT	288
	Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu	
	85 90 95	
20	ATC CAC CAC GAC AGC AAG TGT GAC CCA GGG CAA GCC ACC AAG TAC TTG	336
	Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu	
	100 105 110	
25	TAC GAA CTA CTC TAC AAT GAC CCC ATC AAG ATC ATT CTC ATG CCT GGC	384
	Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly	
	115 120 125	
30	TGT AGT TCT GTC TCC ACA CTT GTA GCT GAG GCT GCC CGG ATG TGG AAC	432
	Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn	
	130 135 140	
35	CTT ATT GTG CTC TCA TAT GGC TCC AGT TCA CCA GCC TTG TCA AAC CGA	480
	Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg	
	145 150 155 160	
40	CAG CGG TTT CCC ACG TTC TTC CGG ACG CAT CCA TCC GCC ACA CTC CAC	528
	Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His	
	165 170 175	
45	AAT CCC ACC CGG GTG AAA CTC TTC GAA AAG TGG GGC TGG AAG AAG ATC	576
	Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile	
	180 185 190	
50	GCT ACC ATC CAA CAG ACC ACC GAG GTC TTC ACC TCA ACG CTG GAT GAC	624
	Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp	
	195 200 205	

	CTG GAG GAG CGA GTG AAA GAG GCT GGG ATC GAG ATC ACT TTC CGA CAG	672
	Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln	
	210 215 220	
5	AGT TTC TTC TCG GAT CCA GCT GTG CCT GTT AAA AAC CTG AAG CGT CAA	720
	Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln	
	225 230 235 240	
10	GAT GCT CGA ATC ATC GTG GGA CTT TTC TAT GAG ACG GAA GCC CGG AAA	768
	Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys	
	245 250 255	
	GTT TTT TGT GAG GTC TAT AAG GAA AGG CTC TTT GGG AAG AAG TAC GTC	816
15	Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val	
	260 265 270	
	TGG TTC CTC ATC GGG TGG TAT GCT GAC AAC TGG TTC AAG ACC TAT GAC	864
20	Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Thr Tyr Asp	
	275 280 285	
	CCG TCA ATC AAT TGT ACA GTG GAA GAA ATG ACC GAG GCG GTG GAG GGC	912
	Pro Ser Ile Asn Cys Thr Val Glu Glu Met Thr Glu Ala Val Glu Gly	
	290 295 300	
25	CAC ATC ACC ACG GAG ATT GTC ATG CTG AAC CCT GCC AAC ACC CGA AGC	960
	His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser	
	305 310 315 320	
30	ATT TCC AAC ATG ACG TCA CAG GAA TTT GTG GAG AAA CTA ACC AAG CGG	1008
	Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg	
	325 330 335	
	CTG AAA AGA CAC CCC GAG GAG ACT GGA GGC TTC CAG GAG GCA CCA CTG	1056
35	Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu	
	340 345 350	
	GCC TAT GAT GCT ATC TGG GCC TTG GCT TTG GCC TTG AAC AAG ACG TCT	1104
40	Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser	
	355 360 365	
	GGA GGA GGT GGT CGT TCC GGC GTG CGC CTG GAG GAC TTT AAC TAC AAC	1152
	Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn	

	370	375	380	
	AAC CAG ACC ATT ACA GAC CAG ATC TAC CGG GCC ATG AAC TCC TCC TCC			1200
	Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser			
5	385	390	395	400
	TTT GAG GGC GTT TCT GGC CAT GTG GTC TTT GAT GCC AGC GGC TCC CGG			1248
	Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg			
	405	410	415	
10	ATG GCA TGG ACA CTT ATC GAG CAG CTA CAG GGC GGC AGC TAC AAG AAG			1296
	Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys			
	420	425	430	
15	ATC GGC TAC TAC GAC AGC ACC AAG GAT GAT CTT TCC TGG TCC AAA ACG			1344
	Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr			
	435	440	445	
	GAC AAG TGG ATT GGA GGG TCT CCC CCA GCT GAC CAG ACC TTG GTC ATC			1392
20	Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile			
	450	455	460	
	AAG ACA TTC CGT TTC CTG TCT CAG AAA CTC TTT ATC TCC GTC TCA GTT			1440
	Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile Ser Val Ser Val			
25	465	470	475	480
	CTC TCC AGC CTG GGC ATT GTT CTT GCT GTT GTC TGT CTG TCC TTT AAC			1488
	Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn			
	485	490	495	
30	ATC TAC AAC TCC CAC GTT CGT TAT ATC CAG AAC TCC CAG CCC AAC CTG			1536
	Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu			
	500	505	510	
35	AAC AAT CTG ACT GCT GTG GGC TGC TCA CTG GCA CTG GCT GCT GTC TTC			1584
	Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu Ala Ala Val Phe			
	515	520	525	
	CCT CTC GGG CTG GAT GGT TAC CAC ATA GGG AGA AGC CAG TTC CCG TTT			1632
40	Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Ser Gln Phe Pro Phe			
	530	535	540	
	GTC TGC CAG GCC CGC CTT TGG CTC TTG GGC TTG GGC TTT AGT CTG GGC			1680

	Val	Cys	Gln	Ala	Arg	Leu	Trp	Leu	Leu	Gly	Leu	Gly	Phe	Ser	Leu	Gly	
	545					550				555						560	
	TAT	GGC	TCT	ATG	TTC	ACC	AAG	ATC	TGG	TGG	GTC	CAC	ACA	GTC	TTC	ACG	1728
5	Tyr	Gly	Ser	Met	Phe	Thr	Lys	Ile	Trp	Trp	Val	His	Thr	Val	Phe	Thr	
					565				570						575		
	AAG	AAG	GAG	GAG	AAG	AAG	GAG	TGG	AGG	AAG	ACC	CTA	GAG	CCC	TGG	AAA	1776
	Lys	Lys	Glu	Glu	Lys	Lys	Glu	Trp	Arg	Lys	Thr	Leu	Glu	Pro	Trp	Lys	
10					580				585						590		
	CTC	TAT	GCC	ACT	GTG	GGC	CTG	CTG	GTG	GGC	ATG	GAT	GTC	CTG	ACT	CTT	1824
	Leu	Tyr	Ala	Thr	Val	Gly	Leu	Leu	Val	Gly	Met	Asp	Val	Leu	Thr	Leu	
					595				600						605		
15	GCC	ATC	TGG	CAG	ATT	GTG	GAC	CCC	TTG	CAC	CGA	ACC	ATT	GAG	ACT	TTT	1872
	Ala	Ile	Trp	Gln	Ile	Val	Asp	Pro	Leu	His	Arg	Thr	Ile	Glu	Thr	Phe	
					610				615						620		
20	GCC	AAG	GAG	GAA	CCA	AAG	GAA	GAC	ATC	GAT	GTC	TCC	ATT	CTG	CCC	CAG	1920
	Ala	Lys	Glu	Glu	Pro	Lys	Glu	Asp	Ile	Asp	Val	Ser	Ile	Leu	Pro	Gln	
					625				630						635		
	TTG	GAG	CAC	TGC	AGC	TCC	AAG	AAG	ATG	AAT	ACG	TGG	CTT	GGC	ATT	TTC	1968
25	Leu	Glu	His	Cys	Ser	Ser	Lys	Lys	Met	Asn	Thr	Trp	Leu	Gly	Ile	Phe	
					645				650						655		
	TAT	GGT	TAC	AAG	GGG	CTG	CTG	CTG	CTG	CTG	GGA	ATC	TTT	CTT	GCT	TAC	2016
	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	Leu	Leu	Gly	Ile	Phe	Leu	Ala	Tyr	
30					660				665						670		
	GAA	ACC	AAG	AGC	GTG	TCC	ACT	GAA	AAG	ATC	AAT	GAC	CAC	AGG	GCC	GTG	2064
	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	Lys	Ile	Asn	Asp	His	Arg	Ala	Val	
					675				680						685		
35	GGC	ATG	GCT	ATC	TAC	AAT	GTC	GCG	GTC	CTG	TGT	CTC	ATC	ACT	GCT	CCT	2112
	Gly	Met	Ala	Ile	Tyr	Asn	Val	Ala	Val	Leu	Cys	Leu	Ile	Thr	Ala	Pro	
					690				695						700		
40	GTG	ACC	ATG	ATC	CTT	TCC	AGT	CAG	CAG	GAC	GCA	GCC	TTT	GCC	TTT	GCC	2160
	Val	Thr	Met	Ile	Leu	Ser	Ser	Gln	Gln	Asp	Ala	Ala	Phe	Ala	Phe	Ala	
					705				710						715		
																720	

	TCT CTG GCC ATC GTG TTC TCT TCC TAC ATC ACT CTG GTT GTG CTC TTT	2208
	Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe	
	725 730 735	
5	GTG CCC AAG ATG CGC AGG CTG ATC ACC CGA GGG GAA TGG CAG TCT GAA	2256
	Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu	
	740 745 750	
	ACG CAG GAC ACC ATG AAA ACA GGA TCA TCC ACC AAC AAC AAC GAG GAA	2304
10	Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu	
	755 760 765	
	GAG AAG TCC CGA CTG TTG GAG AAG GAA AAC CGA GAA CTG GAA AAG ATC	2352
	Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile	
15	770 775 780	
	ATC GCT GAG AAA GAG GAG CGC GTC TCT GAA CTG CGC CAT CAG CTC CAG	2400
	Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln	
	785 790 795 800	
20	TCT CGG CAG CAA CTC CGC TCA CGG CGC CAC CCC CCA ACA CCC CCA GAT	2448
	Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Asp	
	805 810 815	
25	CCC TCT GGG GGC CTT CCC AGG GGA CCC TCT GAG CCC CCT GAC CGG CTT	2496
	Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro Pro Asp Arg Leu	
	820 825 830	
	AGC TGT GAT GGG AGT CGA GTA CAT TTG CTT TAC AAG TGA	2535
30	Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys *	
	835 840	

(2) INFORMATION FOR SEQ ID NO: 47:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 844 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Met Gly Pro Gly Gly Pro Cys Thr Pro Val Gly Trp Pro Leu Pro Leu
 1 5 10 15
 5 Leu Leu Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser
 20 25 30
 Pro His Leu Pro Arg Pro His Pro Arg Val Pro Pro His Pro Ser Ser
 35 40 45
 10 Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly
 50 55 60
 Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu
 15 65 70 75 80
 Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu
 85 90 95
 20 Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu
 100 105 110
 Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly
 115 120 125
 25 Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn
 130 135 140
 Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg
 30 145 150 155 160
 Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His
 165 170 175
 35 Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile
 180 185 190
 Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp
 195 200 205
 40 Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln
 210 215 220

Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln
 225 230 235 240
 Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys
 5 245 250 255
 Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val
 260 265 270
 10 Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Thr Tyr Asp
 275 280 285
 Pro Ser Ile Asn Cys Thr Val Glu Glu Met Thr Glu Ala Val Glu Gly
 290 295 300
 15 His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser
 305 310 315 320
 Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg
 20 325 330 335
 Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu
 340 345 350
 25 Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser
 355 360 365
 Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn
 370 375 380
 30 Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser
 385 390 395 400
 Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg
 35 405 410 415
 Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys
 420 425 430
 40 Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr
 435 440 445
 Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile

	450		455		460														
	Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys	Leu	Phe	Ile	Ser	Val	Ser	Val			
	465					470					475					480			
5	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	Val	Val	Cys	Leu	Ser	Phe	Asn			
					485					490						495			
	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	Gln	Asn	Ser	Gln	Pro	Asn	Leu			
10				500					505					510					
	Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	Leu	Ala	Leu	Ala	Ala	Val	Phe			
			515					520						525					
15	Pro	Leu	Gly	Leu	Asp	Gly	Tyr	His	Ile	Gly	Arg	Ser	Gln	Phe	Pro	Phe			
	530						535					540							
	Val	Cys	Gln	Ala	Arg	Leu	Trp	Leu	Leu	Gly	Leu	Gly	Phe	Ser	Leu	Gly			
	545				550					555						560			
20	Tyr	Gly	Ser	Met	Phe	Thr	Lys	Ile	Trp	Trp	Val	His	Thr	Val	Phe	Thr			
					565					570					575				
	Lys	Lys	Glu	Glu	Lys	Lys	Glu	Trp	Arg	Lys	Thr	Leu	Glu	Pro	Trp	Lys			
25				580					585					590					
	Leu	Tyr	Ala	Thr	Val	Gly	Leu	Leu	Val	Gly	Met	Asp	Val	Leu	Thr	Leu			
			595					600						605					
30	Ala	Ile	Trp	Gln	Ile	Val	Asp	Pro	Leu	His	Arg	Thr	Ile	Glu	Thr	Phe			
	610						615					620							
	Ala	Lys	Glu	Glu	Pro	Lys	Glu	Asp	Ile	Asp	Val	Ser	Ile	Leu	Pro	Gln			
	625					630				635						640			
35	Leu	Glu	His	Cys	Ser	Ser	Lys	Lys	Met	Asn	Thr	Trp	Leu	Gly	Ile	Phe			
				645					650						655				
	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	Leu	Leu	Gly	Ile	Phe	Leu	Ala	Tyr			
40				660					665					670					
	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	Lys	Ile	Asn	Asp	His	Arg	Ala	Val			
			675					680					685						

Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro
 690 695 700
 5 Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala
 705 710 715 720
 Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe
 725 730 735
 10 Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu
 740 745 750
 Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu
 15 755 760 765
 Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile
 770 775 780
 20 Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln
 785 790 795 800
 Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Asp
 805 810 815
 25 Pro Ser Gly Gly Leu Pro Arg Gly Pro Ser Glu Pro Pro Asp Arg Leu
 820 825 830
 Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys
 30 835 840

(2). INFORMATION FOR SEQ ID NO: 48:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2886 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: cDNA to mRNA
 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..2886

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

	ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
	Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
15	1 5 10 15	
	GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
	20 25 30	
20	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
	35 40 45	
25	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
	50 55 60	
	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
30	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
	65 70 75 80	
	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	
35	85 90 95	
	GTC CGA ATC TGC TCC AAG TCT TAT TTG ACC CTG GAA AAT GGG AAG GTT	336
	Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val	
	100 105 110	
40	TTC CTG ACG GGT GGG GAC CTC CCA GCT CTG GAC GGA GCC CGG GTG GAT	384
	Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp	
	115 120 125	

	TTC CGG TGT GAC CCC GAC TTC CAT CTG GTG GGC AGC TCC CGG AGC ATC	432
	Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile	
	130 135 140	
5	TGT AGT CAG GGC CAG TGG AGC ACC CCC AAG CCC CAC TGC CAG GTG AAT	480
	Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn	
	145 150 155 160	
10	CGA ACG CCA CAC TCA GAA CGG CGC GCA GTG TAC ATC GGG GCA CTG TTT	528
	Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe	
	165 170 175	
	CCC ATG AGC GGG GGC TGG CCA GGG GGC CAG GCC TGC CAG CCC GCG GTG	576
15	Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val	
	180 185 190	
	GAG ATG GCG CTG GAG GAC GTG AAT AGC CGC AGG GAC ATC CTG CCG GAC	624
	Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp	
20	195 200 205	
	TAT GAG CTC AAG CTC ATC CAC CAC GAC AGC AAG TGT GAT CCA GGC CAA	672
	Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln	
	210 215 220	
25	GCC ACC AAG TAC CTA TAT GAG CTG CTC TAC AAC GAC CCT ATC AAG ATC	720
	Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile	
	225 230 235 240	
30	ATC CTT ATG CCT GGC TGC AGC TCT GTC TCC ACG CTG GTG GCT GAG GCT	768
	Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala	
	245 250 255	
	GCT AGG ATG TGG AAC CTC ATT GTG CTT TCC TAT GGC TCC AGC TCA CCA	816
35	Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro	
	260 265 270	
	GCC CTG TCA AAC CGG CAG CGT TTC CCC ACT TTC TTC CGA ACG CAC CCA	864
	Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro	
40	275 280 285	
	TCA GCC ACA CTC CAC AAC CCT ACC CGC GTG AAA CTC TTT GAA AAG TGG	912
	Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp	

[illegible]

	Gln	Glu	Ala	Pro	Leu	Ala	Tyr	Asp	Ala	Ile	Trp	Ala	Leu	Ala	Leu	Ala	
	465					470					475					480	
	CTG	AAC	AAG	ACA	TCT	GGA	GGA	GGC	GGC	CGT	TCT	GGT	GTG	CGC	CTG	GAG	1488
5	Leu	Asn	Lys	Thr	Ser	Gly	Gly	Gly	Gly	Arg	Ser	Gly	Val	Arg	Leu	Glu	
					485					490					495		
	GAC	TTC	AAC	TAC	AAC	AAC	CAG	ACC	ATT	ACC	GAC	CAA	ATC	TAC	CGG	GCA	1536
	Asp	Phe	Asn	Tyr	Asn	Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	Arg	Ala	
10				500					505					510			
	ATG	AAC	TCT	TCG	TCC	TTT	GAG	GGT	GTC	TCT	GGC	CAT	GTG	GTG	TTT	GAT	1584
	Met	Asn	Ser	Ser	Ser	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp	
			515					520					525				
15																	
	GCC	AGC	GGC	TCT	CGG	ATG	GCA	TGG	ACG	CTT	ATC	GAG	CAG	CTT	CAG	GGT	1632
	Ala	Ser	Gly	Ser	Arg	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	Gln	Gly	
			530				535					540					
20	GGC	AGC	TAC	AAG	AAG	ATT	GGC	TAC	TAT	GAC	AGC	ACC	AAG	GAT	GAT	CTT	1680
	Gly	Ser	Tyr	Lys	Lys	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	Asp	Leu	
	545					550					555					560	
	TCC	TGG	TCC	AAA	ACA	GAT	AAA	TGG	ATT	GGA	GGG	TCC	CCC	CCA	GCT	GAC	1728
25	Ser	Trp	Ser	Lys	Thr	Asp	Lys	Trp	Ile	Gly	Gly	Ser	Pro	Pro	Ala	Asp	
					565					570					575		
	CAG	ACC	CTG	GTC	ATC	AAG	ACA	TTC	CGC	TTC	CTG	TCA	CAG	AAA	CTC	TTT	1776
	Gln	Thr	Leu	Val	Ile	Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys	Leu	Phe	
30				580					585					590			
	ATC	TCC	GTC	TCA	GTT	CTC	TCC	AGC	CTG	GGC	ATT	GTC	CTA	GCT	GTT	GTC	1824
	Ile	Ser	Val	Ser	Val	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	Val	Val	
			595					600				605					
35																	
	TGT	CTG	TCC	TTT	AAC	ATC	TAC	AAC	TCA	CAT	GTC	CGT	TAT	ATC	CAG	AAC	1872
	Cys	Leu	Ser	Phe	Asn	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	Gln	Asn	
		610					615					620					
40	TCA	CAG	CCC	AAC	CTG	AAC	AAC	CTG	ACT	GCT	GTG	GGC	TGC	TCA	CTG	GCT	1920
	Ser	Gln	Pro	Asn	Leu	Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	Leu	Ala	
	625					630					635				640		

	TTA GCT GCT GTC TTC CCC CTG GGG CTC GAT GGT TAC CAC ATT GGG AGG	1968
	Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg	
	645 650 655	
5	AAC CAG TTT CCT TTC GTC TGC CAG GCC CGC CTC TGG CTC CTG GGC CTG	2016
	Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu	
	660 665 670	
	GGC TTT AGT CTG GGC TAC GGT TCC ATG TTC ACC AAG ATT TGG TGG GTC	2064
10	Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val	
	675 680 685	
	CAC ACG GTC TTC ACA AAG AAG GAA GAA AAG AAG GAG TGG AGG AAG ACT	2112
	His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr	
15	690 695 700	
	CTG GAA CCC TGG AAG CTG TAT GCC ACA GTG GGC CTG CTG GTG GGC ATG	2160
	Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met	
	705 710 715 720	
20	GAT GTC CTC ACT CTC GCC ATC TGG CAG ATC GTG GAC CCT CTG CAC CGG	2208
	Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg	
	725 730 735	
25	ACC ATT GAG ACA TTT GCC AAG GAG GAA CCT AAG GAA GAT ATT GAC GTC	2256
	Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val	
	740 745 750	
	TCT ATT CTG CCC CAG CTG GAG CAT TGC AGC TCC AGG AAG ATG AAT ACA	2304
30	Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr	
	755 760 765	
	TGG CTT GGC ATT TTC TAT GGT TAC AAG GGG CTG CTG CTG CTG CTG GGA	2352
	Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly	
35	770 775 780	
	ATC TTC CTT GCT TAT GAG ACC AAG AGT GTG TCC ACT GAG AAG ATC AAT	2400
	Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn	
	785 790 795 800	
40	GAT CAC CGG GCT GTG GGC ATG GCT ATC TAC AAT GTG GCA GTC CTG TGC	2448
	Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys	
	805 810 815	

	CTC ATC ACT GCT CCT GTC ACC ATG ATT CTG TCC AGC CAG CAG GAT GCA	2496
	Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala	
	820 825 830	
5	GCC TTT GCC TTT GCC TCT CTT GCC ATA GTT TTC TCC TCC TAT ATC ACT	2544
	Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr	
	835 840 845	
10	CTT GTT GTG CTC TTT GTG CCC AAG ATG CGC AGG CTG ATC ACC CGA GGG	2592
	Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly	
	850 855 860	
	GAA TGG CAG TCG GAG GCG CAG GAC ACC ATG AAG ACA GGG TCA TCG ACC	2640
15	Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr	
	865 870 875 880	
	AAC AAC AAC GAG GAG GAG AAG TCC CGG CTG TTG GAG AAG GAG AAC CGT	2688
	Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg	
20	885 890 895	
	GAA CTG GAA AAG ATC ATT GCT GAG AAA GAG GAG CGT GTC TCT GAA CTG	2736
	Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu	
	900 905 910	
25	CGC CAT CAA CTC CAG TCT CGG CAG CAG CTC CGC TCC CGG CGC CAC CCA	2784
	Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro	
	915 920 925	
30	CCG ACA CCC CCA GAA CCC TCT GGG GGC CTG CCC AGG GGA CCC CCT GAG	2832
	Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu	
	930 935 940	
	CCC CCC GAC CGG CTT AGC TGT GAT GGG AGT CGA GTG CAT TTG CTT TAT	2880
35	Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr	
	945 950 955 960	
	AAG TGA	2886
	Lys *	
40		

(2) INFORMATION FOR SEQ ID NO: 49:

H1865-1 WO SEQ

43

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 961 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

10

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 1 5 10 15

15

Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 20 25 30

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 35 40 45

20

Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
 50 55 60

Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
 65 70 75 80

25

Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
 85 90 95

30

Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val
 100 105 110

Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp
 115 120 125

35

Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile
 130 135 140

Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn
 145 150 155 160

40

Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe
 165 170 175

Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val
180 185 190

5 Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp
195 200 205

Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln
210 215 220

10 Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile
225 230 235 240

Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala
245 250 255

15 Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro
260 265 270

20 Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro
275 280 285

Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp
290 295 300

25 Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr
305 310 315 320

Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu
325 330 335

30 Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys
340 345 350

Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu
355 360 365

35 Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe
370 375 380

40 Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp
385 390 395 400

Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr

	405	410	415
	Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro		
	420	425	430
5	Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu		
	435	440	445
	Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe		
10	450	455	460
	Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala		
	465	470	475 480
15	Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu		
	485	490	495
	Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala		
	500	505	510
20	Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp		
	515	520	525
	Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly		
25	530	535	540
	Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu		
	545	550	555 560
30	Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp		
	565	570	575
	Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe		
	580	585	590
35	Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val		
	595	600	605
	Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn		
40	610	615	620
	Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala		
	625	630	635 640

Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg
 645 650 655

5 Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu
 660 665 670

Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val
 675 680 685

10 His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr
 690 695 700

Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met
 15 705 710 715 720

Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg
 725 730 735

20 Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val
 740 745 750

Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr
 755 760 765

25 Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly
 770 775 780

Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn
 30 785 790 795 800

Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys
 805 810 815

35 Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala
 820 825 830

Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr
 835 840 845

40 Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly
 850 855 860

Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr
 865 870 875 880
 Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg
 5 885 890 895
 Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu
 900 905 910
 10 Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro
 915 920 925
 Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu
 930 935 940
 15 Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr
 945 950 955 960
 Lys
 20

(2) INFORMATION FOR SEQ ID NO: 50:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2535 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30
 (ii) MOLECULE TYPE: cDNA to rRNA
 (iii) HYPOTHETICAL: NO
 35 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 40 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..2535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

	ATG GGG CCC GGG GCC CCT TTT GCC CGG GTG GGG TGG CCA CTG CCG CTT	48
	Met Gly Pro Gly Ala Pro Phe Ala Arg Val Gly Trp Pro Leu Pro Leu	
5	1 5 10 15	
	CTG GTT GTG ATG GCG GCA GGG GTG GCT CCG GTG TGG GCC TCC CAC TCC	96
	Leu Val Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser	
	20 25 30	
10	CCC CAT CTC CCG CGG CCT CAC TCG CGG GTC CCC CCG CAC CCC TCC TCA	144
	Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser Ser	
	35 40 45	
15	GAA CGG CGC GCA GTG TAC ATC GGG GCA CTG TTT CCC ATG AGC GGG GGC	192
	Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly	
	50 55 60	
	TGG CCA GGG GGC CAG GCC TGC CAG CCC GCG GTG GAG ATG GCG CTG GAG	240
20	Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu	
	65 70 75 80	
	GAC GTG AAT AGC CGC AGG GAC ATC CTG CCG GAC TAT GAG CTC AAG CTC	288
	Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu	
25	85 90 95	
	ATC CAC CAC GAC AGC AAG TGT GAT CCA GGC CAA GCC ACC AAG TAC CTA	336
	Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu	
	100 105 110	
30	TAT GAG CTG CTC TAC AAC GAC CCT ATC AAG ATC ATC CTT ATG CCT GGC	384
	Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly	
	115 120 125	
35	TGC AGC TCT GTC TCC ACG CTG GTG GCT GAG GCT GCT AGG ATG TGG AAC	432
	Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn	
	130 135 140	
	CTC ATT GTG CTT TCC TAT GGC TCC AGC TCA CCA GCC CTG TCA AAC CGG	480
40	Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg	
	145 150 155 160	
	CAG CGT TTC CCC ACT TTC TTC CGA ACG CAC CCA TCA GCC ACA CTC CAC	528

	Gln	Arg	Phe	Pro	Thr	Phe	Phe	Arg	Thr	His	Pro	Ser	Ala	Thr	Leu	His	
					165					170					175		
	AAC	CCT	ACC	CGC	GTG	AAA	CTC	TTT	GAA	AAG	TGG	GGC	TGG	AAG	AAG	ATT	576
5	Asn	Pro	Thr	Arg	Val	Lys	Leu	Phe	Glu	Lys	Trp	Gly	Trp	Lys	Lys	Ile	
					180					185					190		
	GCT	ACC	ATC	CAG	CAG	ACC	ACT	GAG	GTC	TTC	ACT	TCG	ACT	CTG	GAC	GAC	624
	Ala	Thr	Ile	Gln	Gln	Thr	Thr	Glu	Val	Phe	Thr	Ser	Thr	Leu	Asp	Asp	
10					195					200					205		
	CTG	GAG	GAA	CGA	GTG	AAG	GAG	GCT	GGA	ATT	GAG	ATT	ACT	TTC	CGC	CAG	672
	Leu	Glu	Glu	Arg	Val	Lys	Glu	Ala	Gly	Ile	Glu	Ile	Thr	Phe	Arg	Gln	
					210					215					220		
15																	
	AGT	TTC	TTC	TCA	GAT	CCA	GCT	GTG	CCC	GTC	AAA	AAC	CTG	AAG	CGC	CAG	720
	Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	Val	Lys	Asn	Leu	Lys	Arg	Gln	
					225					230					235		240
20																	
	GAT	GCC	CGA	ATC	ATC	GTG	GGA	CTT	TTC	TAT	GAG	ACT	GAA	GCC	CGG	AAA	768
	Asp	Ala	Arg	Ile	Ile	Val	Gly	Leu	Phe	Tyr	Glu	Thr	Glu	Ala	Arg	Lys	
						245					250				255		
	GTT	TTT	TGT	GAG	GTG	TAC	AAG	GAG	CGT	CTC	TTT	GGG	AAG	AAG	TAC	GTC	816
25	Val	Phe	Cys	Glu	Val	Tyr	Lys	Glu	Arg	Leu	Phe	Gly	Lys	Lys	Tyr	Val	
					260					265					270		
	TGG	TTC	CTC	ATT	GGG	TGG	TAT	GCT	GAC	AAT	TGG	TTC	AAG	ATC	TAC	GAC	864
	Trp	Phe	Leu	Ile	Gly	Trp	Tyr	Ala	Asp	Asn	Trp	Phe	Lys	Ile	Tyr	Asp	
30					275					280					285		
	CCT	TCT	ATC	AAC	TGC	ACA	GTG	GAT	GAG	ATG	ACT	GAG	GCG	GTG	GAG	GGC	912
	Pro	Ser	Ile	Asn	Cys	Thr	Val	Asp	Glu	Met	Thr	Glu	Ala	Val	Glu	Gly	
					290					295					300		
35																	
	CAC	ATC	ACA	ACT	GAG	ATT	GTC	ATG	CTG	AAT	CCT	GCC	AAT	ACC	CGC	AGC	960
	His	Ile	Thr	Thr	Glu	Ile	Val	Met	Leu	Asn	Pro	Ala	Asn	Thr	Arg	Ser	
					305					310					315		320
40																	
	ATT	TCC	AAC	ATG	ACA	TCC	CAG	GAA	TTT	GTG	GAG	AAA	CTA	ACC	AAG	CGA	1008
	Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	Phe	Val	Glu	Lys	Leu	Thr	Lys	Arg	
						325					330				335		

	CTG AAA AGA CAC CCT GAG GAG ACA GGA GGC TTC CAG GAG GCA CCG CTG	1056
	Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu	
	340 345 350	
5	GCC TAT GAT GCC ATC TGG GCC TTG GCA CTG GCC CTG AAC AAG ACA TCT	1104
	Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser	
	355 360 365	
	GGA GGA GGC GGC CGT TCT GGT GTG CGC CTG GAG GAC TTC AAC TAC AAC	1152
10	Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn	
	370 375 380	
	AAC CAG ACC ATT ACC GAC CAA ATC TAC CGG GCA ATG AAC TCT TCG TCC	1200
	Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser	
15	385 390 395 400	
	TTT GAG GGT GTC TCT GGC CAT GTG GTG TTT GAT GCC AGC GGC TCT CGG	1248
	Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg	
	405 410 415	
20	ATG GCA TGG ACG CTT ATC GAG CAG CTT CAG GGT GGC AGC TAC AAG AAG	1296
	Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys	
	420 425 430	
25	ATT GGC TAC TAT GAC AGC ACC AAG GAT GAT CTT TCC TGG TCC AAA ACA	1344
	Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr	
	435 440 445	
	GAT AAA TGG ATT GGA GGG TCC CCC CCA GCT GAC CAG ACC CTG GTC ATC	1392
30	Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile	
	450 455 460	
	AAG ACA TTC CGC TTC CTG TCA CAG AAA CTC TTT ATC TCC GTC TCA GTT	1440
	Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile Ser Val Ser Val	
35	465 470 475 480	
	CTC TCC AGC CTG GGC ATT GTC CTA GCT GTT GTC TGT CTG TCC TTT AAC	1488
	Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn	
	485 490 495	
40	ATC TAC AAC TCA CAT GTC CGT TAT ATC CAG AAC TCA CAG CCC AAC CTG	1536
	Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu	
	500 505 510	

	AAC AAC CTG ACT GCT GTG GGC TGC TCA CTG GCT TTA GCT GCT GTC TTC	1584
	Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu Ala Ala Val Phe	
	515 520 525	
5	CCC CTG GGG CTC GAT GGT TAC CAC ATT GGG AGG AAC CAG TTT CCT TTC	1632
	Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Asn Gln Phe Pro Phe	
	530 535 540	
10	GTC TGC CAG GCC CGC CTC TGG CTC CTG GGC CTG GGC TTT AGT CTG GGC	1680
	Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly	
	545 550 555 560	
	TAC GGT TCC ATG TTC ACC AAG ATT TGG TGG GTC CAC ACG GTC TTC ACA	1728
15	Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr	
	565 570 575	
	AAG AAG GAA GAA AAG AAG GAG TGG AGG AAG ACT CTG GAA CCC TGG AAG	1776
	Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys	
20	580 585 590	
	CTG TAT GCC ACA GTG GGC CTG CTG GTG GGC ATG GAT GTC CTC ACT CTC	1824
	Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu	
	595 600 605	
25	GCC ATC TGG CAG ATC GTG GAC CCT CTG CAC CGG ACC ATT GAG ACA TTT	1872
	Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe	
	610 615 620	
30	GCC AAG GAG GAA CCT AAG GAA GAT ATT GAC GTC TCT ATT CTG CCC CAG	1920
	Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln	
	625 630 635 640	
	CTG GAG CAT TGC AGC TCC AGG AAG ATG AAT ACA TGG CTT GGC ATT TTC	1968
35	Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr Trp Leu Gly Ile Phe	
	645 650 655	
	TAT GGT TAC AAG GGG CTG CTG CTG CTG CTG GGA ATC TTC CTT GCT TAT	2016
	Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr	
40	660 665 670	
	GAG ACC AAG AGT GTG TCC ACT GAG AAG ATC AAT GAT CAC CGG GCT GTG	2064
	Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val	

	675	680	685	
	GGC ATG GCT ATC TAC AAT GTG GCA GTC CTG TGC CTC ATC ACT GCT CCT	2112		
	Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro			
5	690 695 700			
	GTC ACC ATG ATT CTG TCC AGC CAG CAG GAT GCA GCC TTT GCC TTT GCC	2160		
	Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala			
	705 710 715 720			
10	TCT CTT GCC ATA GTT TTC TCC TCC TAT ATC ACT CTT GTT GTG CTC TTT	2208		
	Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe			
	725 730 735			
15	GTG CCC AAG ATG CGC AGG CTG ATC ACC CGA GGG GAA TGG CAG TCG GAG	2256		
	Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu			
	740 745 750			
	GCG CAG GAC ACC ATG AAG ACA GGG TCA TCG ACC AAC AAC AAC GAG GAG	2304		
20	Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu			
	755 760 765			
	GAG AAG TCC CGG CTG TTG GAG AAG GAG AAC CGT GAA CTG GAA AAG ATC	2352		
	Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile			
25	770 775 780			
	ATT GCT GAG AAA GAG GAG CGT GTC TCT GAA CTG CGC CAT CAA CTC CAG	2400		
	Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln			
	785 790 795 800			
30	TCT CGG CAG CAG CTC CGC TCC CGG CGC CAC CCA CCG ACA CCC CCA GAA	2448		
	Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu			
	805 810 815			
35	CCC TCT GGG GGC CTG CCC AGG GGA CCC CCT GAG CCC CCC GAC CGG CTT	2496		
	Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu			
	820 825 830			
	AGC TGT GAT GGG AGT CGA GTG CAT TTG CTT TAT AAG TGA	2535		
40	Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys *			
	835 840			

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 844 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Met Gly Pro Gly Ala Pro Phe Ala Arg Val Gly Trp Pro Leu Pro Leu
 1 5 10 15
 Leu Val Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser
 20 25 30
 Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser Ser
 35 40 45
 Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly
 50 55 60
 Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu
 65 70 75 80
 Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu
 85 90 95
 Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu
 100 105 110
 Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly
 115 120 125
 Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn
 130 135 140
 Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg
 145 150 155 160
 Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His
 165 170 175

Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile
 180 185 190

5 Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp
 195 200 205

Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln
 210 215 220

10 Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln
 225 230 235 240

Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys
 15 245 250 255

Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val
 260 265 270

20 Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp
 275 280 285

Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly
 290 295 300

25 His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser
 305 310 315 320

Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg
 30 325 330 335

Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu
 340 345 350

35 Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser
 355 360 365

Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn
 370 375 380

40 Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser
 385 390 395 400

Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg
 405 410 415
 Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys
 5 420 425 430
 Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr
 435 440 445
 10 Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile
 450 455 460
 Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile Ser Val Ser Val
 465 470 475 480
 15 Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn
 485 490 495
 Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu
 20 500 505 510
 Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu Ala Ala Val Phe
 515 520 525
 25 Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Asn Gln Phe Pro Phe
 530 535 540
 Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly
 545 550 555 560
 30 Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr
 565 570 575
 Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys
 35 580 585 590
 Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu
 595 600 605
 40 Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe
 610 615 620
 Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln

	625		630		635		640									
	Leu	Glu	His	Cys	Ser	Ser	Arg	Lys	Met	Asn	Thr	Trp	Leu	Gly	Ile	Phe
					645					650					655	
5	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	Leu	Leu	Gly	Ile	Phe	Leu	Ala	Tyr
				660					665					670		
	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	Lys	Ile	Asn	Asp	His	Arg	Ala	Val
10			675					680					685			
	Gly	Met	Ala	Ile	Tyr	Asn	Val	Ala	Val	Leu	Cys	Leu	Ile	Thr	Ala	Pro
		690				695					700					
15	Val	Thr	Met	Ile	Leu	Ser	Ser	Gln	Gln	Asp	Ala	Ala	Phe	Ala	Phe	Ala
	705				710					715					720	
	Ser	Leu	Ala	Ile	Val	Phe	Ser	Ser	Tyr	Ile	Thr	Leu	Val	Val	Leu	Phe
				725					730					735		
20	Val	Pro	Lys	Met	Arg	Arg	Leu	Ile	Thr	Arg	Gly	Glu	Trp	Gln	Ser	Glu
			740					745					750			
	Ala	Gln	Asp	Thr	Met	Lys	Thr	Gly	Ser	Ser	Thr	Asn	Asn	Asn	Glu	Glu
25		755				760						765				
	Glu	Lys	Ser	Arg	Leu	Leu	Glu	Lys	Glu	Asn	Arg	Glu	Leu	Glu	Lys	Ile
		770				775						780				
30	Ile	Ala	Glu	Lys	Glu	Glu	Arg	Val	Ser	Glu	Leu	Arg	His	Gln	Leu	Gln
	785				790					795					800	
	Ser	Arg	Gln	Gln	Leu	Arg	Ser	Arg	Arg	His	Pro	Pro	Thr	Pro	Pro	Glu
				805					810					815		
35	Pro	Ser	Gly	Gly	Leu	Pro	Arg	Gly	Pro	Pro	Glu	Pro	Pro	Asp	Arg	Leu
				820					825					830		
	Ser	Cys	Asp	Gly	Ser	Arg	Val	His	Leu	Leu	Tyr	Lys				
40		835				840										

(2) INFORMATION FOR SEQ ID NO: 52:

(D) TOPOLOGY: linear

(B) LOCATION:1..2895

GTC CGA AAG TGC CTG GCC AAT GGC TCC TGG ACA GAT ATG GAC ACA CCC 288

	Val	Arg	Lys	Cys	Leu	Ala	Asn	Gly	Ser	Trp	Thr	Asp	Met	Asp	Thr	Pro	
					85					90					95		
	AGC	CGC	TGT	GTC	CGA	ATC	TGT	TCC	AAG	TCA	TAT	TTG	GCC	CTG	GAA	AAT	336
5	Ser	Arg	Cys	Val	Arg	Ile	Cys	Ser	Lys	Ser	Tyr	Leu	Ala	Leu	Glu	Asn	
				100					105					110			
	GGG	AAG	GTC	TTC	CTG	ACG	GGT	GGG	GAC	CTC	CCC	GCT	CTG	GAT	GGA	GCC	384
10	Gly	Lys	Val	Phe	Leu	Thr	Gly	Gly	Asp	Leu	Pro	Ala	Leu	Asp	Gly	Ala	
			115					120					125				
	CGG	GTG	GAT	TTC	CGG	TGT	GAC	CCT	GAC	TTC	CAT	CTT	GTG	GGC	AGC	TCC	432
	Arg	Val	Asp	Phe	Arg	Cys	Asp	Pro	Asp	Phe	His	Leu	Val	Gly	Ser	Ser	
			130				135					140					
15	CGG	AGT	ATC	TGT	AGT	CAG	GGC	CAG	TGG	AGC	ACT	CCC	AAG	CCC	CAC	TGC	480
	Arg	Ser	Ile	Cys	Ser	Gln	Gly	Gln	Trp	Ser	Thr	Pro	Lys	Pro	His	Cys	
	145					150				155						160	
20	CAG	GTG	AGC	CGA	ACG	CCG	CAC	TCA	GAG	CGG	CGA	GCG	GTG	TAC	ATC	GGG	528
	Gln	Val	Ser	Arg	Thr	Pro	His	Ser	Glu	Arg	Arg	Ala	Val	Tyr	Ile	Gly	
					165					170				175			
	GCG	CTG	TTT	CCC	ATG	AGC	GGG	GGC	TGG	CCG	GGG	GGC	CAG	GCC	TGC	CAG	576
25	Ala	Leu	Phe	Pro	Met	Ser	Gly	Gly	Trp	Pro	Gly	Gly	Gln	Ala	Cys	Gln	
				180					185					190			
	CCC	GCG	GTG	GAG	ATG	GCG	CTG	GAG	GAC	GTG	AAT	AGC	CGC	AGG	GAC	ATC	624
30	Pro	Ala	Val	Glu	Met	Ala	Leu	Glu	Asp	Val	Asn	Ser	Arg	Arg	Asp	Ile	
			195					200					205				
	CTG	CCG	GAC	TAC	GAG	CTC	AAG	CTC	ATC	CAC	CAC	GAC	AGC	AAG	TGT	GAC	672
	Leu	Pro	Asp	Tyr	Glu	Leu	Lys	Leu	Ile	His	His	Asp	Ser	Lys	Cys	Asp	
			210				215					220					
35	CCA	GGC	CAA	GCT	ACC	AAG	TAC	CTG	TAT	GAA	CTG	CTC	TAC	AAC	GAC	CCC	720
	Pro	Gly	Gln	Ala	Thr	Lys	Tyr	Leu	Tyr	Glu	Leu	Leu	Tyr	Asn	Asp	Pro	
	225					230					235				240		
40	ATC	AAG	ATC	ATC	CTC	ATG	CCT	GGC	TGC	AGC	TCT	GTC	TCC	ACG	CTT	GTG	768
	Ile	Lys	Ile	Ile	Leu	Met	Pro	Gly	Cys	Ser	Ser	Val	Ser	Thr	Leu	Val	
					245				250						255		

	GCT GAG GCT GCC AGG ATG TGG AAC CTC ATT GTG CTC TCC TAT GGT TCC	816
	Ala Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser	
	260 265 270	
5	AGC TCA CCA GCT CTG TCC AAC CGG CAG CGC TTT CCT ACC TTC TTC CGA	864
	Ser Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg	
	275 280 285	
	ACT CAT CCC TCG GCC ACG CTC CAC AAC CCT ACG CGA GTG AAG CTC TTT	912
10	Thr His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe	
	290 295 300	
	GAG AAG TGG GGC TGG AGG AAG ATT GCC ACC ATC CAG CAG ACC ACC GAG	960
	Glu Lys Trp Gly Trp Arg Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu	
15	305 310 315 320	
	GTG TTC ACA TCG ACT CTG GAC GAC CTA GAG GAA CGA GTG AAG GAG GCT	1008
	Val Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala	
	325 330 335	
20	GGG ATT GAG ATT ACT TTC CGC CAG AGC TTC TTC TCA GAT CCT GCC GTG	1056
	Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val	
	340 345 350	
25	CCT GTC AAG AAC CTC AAG CGC CAG GAT GCC CGA ATC ATC GTG GGA CTT	1104
	Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu	
	355 360 365	
	TTC TAT GAG ACT GAA GCC CGG AAA GTG TTC TGT GAG GTA TAC AAG GAG	1152
30	Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu	
	370 375 380	
	CGG CTC TTT GGG AAG AAG TAT GTG TGG TTC CTC ATT GGG TGG TAT GCT	1200
	Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala	
35	385 390 395 400	
	GAC AAT TGG TTC AAG ACC TAC GAC CCC TCC ATC AAC TGC ACA GTG GAT	1248
	Asp Asn Trp Phe Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp	
	405 410 415	
40	GAG ATG ACC GAG GCT GTG GAA GGC CAC ATC ACC ACT GAG ATT GTC ATG	1296
	Glu Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met	
	420 425 430	

	CTG AAC CCA GCC AAC ACC CGC AGC ATC TCC AAC ATG ACA TCC CAG GAG	1344
	Leu Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu	
	435 440 445	
5	TTT GTG GAG AAA CTG ACC AAG AGA CTC AAG AGA CAC CCT GAG GAG ACA	1392
	Phe Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr	
	450 455 460	
10	GGC GGC TTC CAG GAG GCA CCG CTG GCC TAT GAT GCC ATC TGG GCC TTG	1440
	Gly Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu	
	465 470 475 480	
15	GCA TTG GCC CTG AAC AAG ACA TCT GGA GGG AGC GGC CGT TCG GGG GTG	1488
	Ala Leu Ala Leu Asn Lys Thr Ser Gly Gly Ser Gly Arg Ser Gly Val	
	485 490 495	
20	CGC CTG GAA GAC TTC AAC TAC AAC AAC CAG ACG ATC ACA GAC CAA ATC	1536
	Arg Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile	
	500 505 510	
25	TAC CGC GCA ATG AAC TCC TCG TCC TTT GAG GGT GTC TCT GGC CAC GTG	1584
	Tyr Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val	
	515 520 525	
30	GTG TTT GAT GCC AGC GGC TCA CGG ATG GCC TGG ACT CTG ATT GAG CAG	1632
	Val Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln	
	530 535 540	
35	CTG CAG GGT GGC AGC TAC AAG AAG ATC GGC TAC TAT GAC AGC ACC AAG	1680
	Leu Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys	
	545 550 555 560	
40	GAT GAC CTT TCC TGG TCT AAA ACG GAC AAA TGG ATT GGA GGG GCC CCC	1728
	Asp Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ala Pro	
	565 570 575	
45	CCG GCC GAC CAG ACC CTG GTC ATC AAG ACA TTT CGC TTC ATG TCA CAG	1776
	Pro Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Met Ser Gln	
	580 585 590	
50	AAG CTC TTC ATT TCA GTC TCT GTC CTC TCC AGC CTG GGC ATT GTC CTG	1824
	Lys Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu	

	595	600	605	
	GCT GTG GTC TGT CTG TCC TTT AAC ATC TAC AAC TCT CAT GTC CGT TAC	1872		
	Ala Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr			
5	610	615	620	
	ATC CAG AAC TCC CAG CCC AAC TTG AAC AAT CTG ACT GCT GTG GGC TGC	1920		
	Ile Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys			
	625	630	635	640
10	TCC CTG GCA TTG GCT GCC GTC TTC CCC CTG GGG CTA GAT GGG TAC CAC	1968		
	Ser Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His			
	645	650	655	
15	ATC GGG AGA AGC CAG TTT CCT TTT GTG TGT CAG GCA CGC CTC TGG CTC	2016		
	Ile Gly Arg Ser Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu			
	660	665	670	
	CTG GGT CTG GGC TTC AGT CTG GGC TAT GGC TCC ATG TTC ACG AAG ATC	2064		
20	Leu Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile			
	675	680	685	
	TGG TGG GTC CAC ACG GTC TTC ACT AAG AAG GAG GAG AAG AAG GAG TGG	2112		
	Trp Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp			
25	690	695	700	
	AGG AAG ACC CTG GAG CCC TGG AAG CTG TAC ACC ACA GTG GGC TTG CTA	2160		
	Arg Lys Thr Leu Glu Pro Trp Lys Leu Tyr Thr Thr Val Gly Leu Leu			
	705	710	715	720
30	GTG GGC ATG GAT GTC CTC ACT CTT GCC ATT TGG CAG ATG GTA GAC CCC	2208		
	Val Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Met Val Asp Pro			
	725	730	735	
35	TTG CAC CGG ACC ATT GAG ACT TTT GCC AAG GAG GAA CCA AAG GAA GAT	2256		
	Leu His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp			
	740	745	750	
	ATT GAT GTG TCC ATC CTG CCC CAG CTG GAG CAC TGC AGC TCC AAG AAA	2304		
40	Ile Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Lys Lys			
	755	760	765	
	ATG AAC ACC TGG CTT GGC ATT TTC TAT GGT TAC AAG GGG CTG CTG CTG	2352		

	Met	Asn	Thr	Trp	Leu	Gly	Ile	Phe	Tyr	Gly	Tyr	Lys	Gly	Leu	Leu	Leu	
	770						775					780					
	CTG	CTA	GGC	ATC	TTT	CTT	GCT	TAT	GAG	ACC	AAG	AGC	GTG	TCT	ACT	GAG	2400
5	Leu	Leu	Gly	Ile	Phe	Leu	Ala	Tyr	Glu	Thr	Lys	Ser	Val	Ser	Thr	Glu	
	785					790					795					800	
	AAG	ATC	AAT	GAC	CAC	CGG	GCT	GTG	GGC	ATG	GCC	ATG	TAC	AAC	GTG	GCG	2448
	Lys	Ile	Asn	Asp	His	Arg	Ala	Val	Gly	Met	Ala	Met	Tyr	Asn	Val	Ala	
10					805					810					815		
	GTC	CTG	TGC	CTC	ATC	ACT	GCC	CCG	GTC	ACC	ATG	ATC	CTG	TCC	AGC	CAG	2496
	Val	Leu	Cys	Leu	Ile	Thr	Ala	Pro	Val	Thr	Met	Ile	Leu	Ser	Ser	Gln	
				820					825					830			
15																	
	CAG	GAT	GCA	GCT	TTC	GCC	TTT	GCA	GCT	CTT	GCC	ATA	GTG	TTC	TCC	TCC	2544
	Gln	Asp	Ala	Ala	Phe	Ala	Phe	Ala	Ala	Leu	Ala	Ile	Val	Phe	Ser	Ser	
			835					840					845				
20																	
	TAC	ATC	ACT	CTG	GTC	GTT	CTG	TTC	GTG	CCG	AAG	ATG	CGC	AGG	TTG	ATC	2592
	Tyr	Ile	Thr	Leu	Val	Val	Leu	Phe	Val	Pro	Lys	Met	Arg	Arg	Leu	Ile	
		850					855					860					
	ACC	CGG	GGT	GAG	TGG	CAG	TCG	GAG	GCG	CAG	GAT	ACC	ATG	AAA	ACG	GGG	2640
25	Thr	Arg	Gly	Glu	Trp	Gln	Ser	Glu	Ala	Gln	Asp	Thr	Met	Lys	Thr	Gly	
	865					870					875					880	
	TCG	TCG	ACC	AAC	AAC	AAT	GAG	GAA	GAG	AAG	TCC	CGA	CTG	TTG	GAG	AAG	2688
	Ser	Ser	Thr	Asn	Asn	Asn	Glu	Glu	Glu	Lys	Ser	Arg	Leu	Leu	Glu	Lys	
30					885					890					895		
	GAG	AAC	CGG	GAG	CTG	GAG	AAG	ATC	ATT	GCT	GAG	AAA	GAG	GAG	CGA	GTG	2736
	Glu	Asn	Arg	Glu	Leu	Glu	Lys	Ile	Ile	Ala	Glu	Lys	Glu	Glu	Arg	Val	
				900						905					910		
35																	
	TCC	GAG	CTG	CGC	CAT	CAG	CTT	CGT	TCT	CGG	CAG	CAG	CTG	CGC	CCT	CGG	2784
	Ser	Glu	Leu	Arg	His	Gln	Leu	Arg	Ser	Arg	Gln	Gln	Leu	Arg	Pro	Arg	
			915					920					925				
40																	
	CGT	CAC	CCC	CCG	ACG	CCC	CCA	GAC	CCC	TCA	GGG	GGC	CTG	CCC	AGG	GGA	2832
	Arg	His	Pro	Pro	Thr	Pro	Pro	Asp	Pro	Ser	Gly	Gly	Leu	Pro	Arg	Gly	
		930						935				940					

CCC CAT GAG CCC CCT GAC CGG CTC AGC TGT GAC GGG AGC CGG GTT CAC 2880
 Pro His Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His
 945 950 955 960

5 TTG CTG TAC AAG TGA 2895
 Leu Leu Tyr Lys *
 965

10 (2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 964 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

20 Met Leu Leu Leu Leu Leu Pro Leu Ala Leu Ala Pro Leu Phe Leu Arg
 1 5 10 15
 Pro Pro Gly Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly
 25 20 25 30
 Cys Gln Ile Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly
 35 40 45
 30 Leu Thr Arg Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr
 50 55 60
 Glu Ile Glu Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys
 65 70 75 80
 35 Val Arg Lys Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro
 85 90 95
 Ser Arg Cys Val Arg Ile Cys Ser Lys Ser Tyr Leu Ala Leu Glu Asn
 40 100 105 110
 Gly Lys Val Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala
 115 120 125

Arg Val Asp Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser
 130 135 140

5 Arg Ser Ile Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys
 145 150 155 160

Gln Val Ser Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly
 165 170 175

10 Ala Leu Phe Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln
 180 185 190

Pro Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile
 15 195 200 205

Leu Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp
 210 215 220

20 Pro Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro
 225 230 235 240

Ile Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val
 245 250 255

25 Ala Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser
 260 265 270

Ser Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg
 30 275 280 285

Thr His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe
 290 295 300

35 Glu Lys Trp Gly Trp Arg Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu
 305 310 315 320

Val Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala
 325 330 335

40 Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val
 340 345 350

Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu
 355 360 365

Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu
 5 370 375 380

Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala
 385 390 395 400

Asp Asn Trp Phe Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp
 10 405 410 415

Glu Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met
 420 425 430

15 Leu Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu
 435 440 445

Phe Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr
 20 450 455 460

Gly Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu
 465 470 475 480

25 Ala Leu Ala Leu Asn Lys Thr Ser Gly Gly Ser Gly Arg Ser Gly Val
 485 490 495

Arg Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile
 500 505 510

30 Tyr Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val
 515 520 525

Val Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln
 35 530 535 540

Leu Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys
 545 550 555 560

40 Asp Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ala Pro
 565 570 575

Pro Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Met Ser Gln

	580	585	590
	Lys Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu		
	595	600	605
5	Ala Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr		
	610	615	620
	Ile Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys		
10	625	630	635 640
	Ser Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His		
	645	650	655
15	Ile Gly Arg Ser Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu		
	660	665	670
	Leu Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile		
	675	680	685
20	Trp Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp		
	690	695	700
	Arg Lys Thr Leu Glu Pro Trp Lys Leu Tyr Thr Thr Val Gly Leu Leu		
25	705	710	715 720
	Val Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Met Val Asp Pro		
	725	730	735
30	Leu His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp		
	740	745	750
	Ile Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Lys Lys		
	755	760	765
35	Met Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu		
	770	775	780
	Leu Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu		
40	785	790	795 800
	Lys Ile Asn Asp His Arg Ala Val Gly Met Ala Met Tyr Asn Val Ala		
	805	810	815

Val Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln
820 825 830

5 Gln Asp Ala Ala Phe Ala Phe Ala Ala Leu Ala Ile Val Phe Ser Ser
835 840 845

Tyr Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile
850 855 860

10 Thr Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly
865 870 875 880

Ser Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys
15 885 890 895

Glu Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val
900 905 910

20 Ser Glu Leu Arg His Gln Leu Arg Ser Arg Gln Gln Leu Arg Pro Arg
915 920 925

Arg His Pro Pro Thr Pro Pro Asp Pro Ser Gly Gly Leu Pro Arg Gly
930 935 940

25 Pro His Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His
945 950 955 960

Leu Leu Tyr Lys

30

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1737 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

5

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..1737

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
1 5 10 15	
GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
20 25 30	
ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
35 40 45	
GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
50 55 60	
TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
65 70 75 80	
TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288
Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	
85 90 95	
GTC CGA ATC TGC TCC AAG TCT TAT TTG ACC CTG GAA AAT GGG AAG GTT	336
Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val	
100 105 110	
TTC CTG ACG GGT GGG GAC CTC CCA GCT CTG GAC GGA GCC CGG GTG GAT	384
Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp	
115 120 125	

	TTC CGG TGT GAC CCC GAC TTC CAT CTG GTG GGC AGC TCC CGG AGC ATC	432
	Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile	
	130 135 140	
5	TGT AGT CAG GGC CAG TGG AGC ACC CCC AAG CCC CAC TGC CAG GTG AAT	480
	Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn	
	145 150 155 160	
	CGA ACG CCA CAC TCA GAA CGG CGC GCA GTG TAC ATC GGG GCA CTG TTT	528
10	Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe	
	165 170 175	
	CCC ATG AGC GGG GGC TGG CCA GGG GGC CAG GCC TGC CAG CCC GCG GTG	576
	Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val	
15	180 185 190	
	GAG ATG GCG CTG GAG GAC GTG AAT AGC CGC AGG GAC ATC CTG CCG GAC	624
	Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp	
	195 200 205	
20	TAT GAG CTC AAG CTC ATC CAC CAC GAC AGC AAG TGT GAT CCA GGC CAA	672
	Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln	
	210 215 220	
25	GCC ACC AAG TAC CTA TAT GAG CTG CTC TAC AAC GAC CCT ATC AAG ATC	720
	Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile	
	225 230 235 240	
	ATC CTT ATG CCT GGC TGC AGC TCT GTC TCC ACG CTG GTG GCT GAG GCT	768
30	Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala	
	245 250 255	
	GCT AGG ATG TGG AAC CTC ATT GTG CTT TCC TAT GGC TCC AGC TCA CCA	816
	Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro	
35	260 265 270	
	GCC CTG TCA AAC CGG CAG CGT TTC CCC ACT TTC TTC CGA ACG CAC CCA	864
	Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro	
	275 280 285	
40	TCA GCC ACA CTC CAC AAC CCT ACC CGC GTG AAA CTC TTT GAA AAG TGG	912
	Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp	
	290 295 300	

	GGC TGG AAG AAG ATT GCT ACC ATC CAG CAG ACC ACT GAG GTC TTC ACT	960
	Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr	
	305 310 315 320	
5	TCG ACT CTG GAC GAC CTG GAG GAA CGA GTG AAG GAG GCT GGA ATT GAG	1008
	Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu	
	325 330 335	
10	ATT ACT TTC CGC CAG AGT TTC TTC TCA GAT CCA GCT GTG CCC GTC AAA	1056
	Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys	
	340 345 350	
	AAC CTG AAG CGC CAG GAT GCC CGA ATC ATC GTG GGA CTT TTC TAT GAG	1104
15	Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu	
	355 360 365	
	ACT GAA GCC CGG AAA GTT TTT TGT GAG GTG TAC AAG GAG CGT CTC TTT	1152
	Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe	
20	370 375 380	
	GGG AAG AAG TAC GTC TGG TTC CTC ATT GGG TGG TAT GCT GAC AAT TGG	1200
	Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp	
	385 390 395 400	
25	TTC AAG ATC TAC GAC CCT TCT ATC AAC TGC ACA GTG GAT GAG ATG ACT	1248
	Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr	
	405 410 415	
30	GAG GCG GTG GAG GGC CAC ATC ACA ACT GAG ATT GTC ATG CTG AAT CCT	1296
	Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro	
	420 425 430	
	GCC AAT ACC CGC AGC ATT TCC AAC ATG ACA TCC CAG GAA TTT GTG GAG	1344
35	Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu	
	435 440 445	
	AAA CTA ACC AAG CGA CTG AAA AGA CAC CCT GAG GAG ACA GGA GGC TTC	1392
	Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe	
40	450 455 460	
	CAG GAG GCA CCG CTG GCC TAT GAT GCC ATC TGG GCC TTG GCA CTG GCC	1440
	Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala	

	465	470	475	480	
	CTG AAC AAG ACA TCT GGA GGA GGC GGC CGT TCT GGT GTG CGC CTG GAG				1488
	Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu				
5		485	490	495	
	GAC TTC AAC TAC AAC AAC CAG ACC ATT ACC GAC CAA ATC TAC CGG GCA				1536
	Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala				
		500	505	510	
10	ATG AAC TCT TCG TCC TTT GAG GGT GTC TCT GGC CAT GTG GTG TTT GAT				1584
	Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp				
		515	520	525	
15	GCC AGC GGC TCT CGG ATG GCA TGG ACG CTT ATC GAG CAG CTT CAG GGT				1632
	Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly				
		530	535	540	
	GGC AGC TAC AAG AAG ATT GGC TAC TAT GAC AGC ACC AAG GAT GAT CTT				1680
20	Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu				
		545	550	555	560
	TCC TGG TCC AAA ACA GAT AAA TGG ATT GTT ATA TCC AGA ACT CAC AGC				1728
	Ser Trp Ser Lys Thr Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser				
25		565	570	575	
	CCA ACC TGA				1737
	Pro Thr *				

30

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 578 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly

	1		5		10		15
	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile						
		20		25		30	
5	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg						
		35		40		45	
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu						
10		50		55		60	
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys						
		65		70		75	80
15	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys						
			85		90		95
	Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val						
		100		105		110	
20	Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp						
		115		120		125	
	Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile						
25		130		135		140	
	Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn						
		145		150		155	160
30	Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe						
			165		170		175
	Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val						
		180		185		190	
35	Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp						
		195		200		205	
	Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln						
40		210		215		220	
	Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile						
		225		230		235	240

Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala
 245 250 255

5 Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro
 260 265 270

Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro
 275 280 285

10 Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp
 290 295 300

Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr
 15 305 310 315 320

Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu
 325 330 335

20 Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys
 340 345 350

Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu
 355 360 365

25 Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe
 370 375 380

Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp
 30 385 390 395 400

Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr
 405 410 415

35 Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro
 420 425 430

Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu
 435 440 445

40 Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe
 450 455 460

Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala
465 470 475 480

Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu
5 485 490 495

Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala
500 505 510

Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp
10 515 520 525

Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly
530 535 540

Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu
15 545 550 555 560

Ser Trp Ser Lys Thr Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser
20 565 570 575

Pro Thr

25

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 1386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..1386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

5	ATG GGG CCC GGG GCC CCT TTT GCC CGG GTG GGG TGG CCA CTG CCG CTT	48
	Met Gly Pro Gly Ala Pro Phe Ala Arg Val Gly Trp Pro Leu Pro Leu	
	1 5 10 15	
10	CTG GTT GTG ATG GCG GCA GGG GTG GCT CCG GTG TGG GCC TCC CAC TCC	96
	Leu Val Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser	
	20 25 30	
15	CCC CAT CTC CCG CGG CCT CAC TCG CGG GTC CCC CCG CAC CCC TCC TCA	144
	Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser Ser	
	35 40 45	
20	GAA CGG CGC GCA GTG TAC ATC GGG GCA CTG TTT CCC ATG AGC GGG GGC	192
	Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly	
	50 55 60	
25	TGG CCA GGG GGC CAG GCC TGC CAG CCC GCG GTG GAG ATG GCG CTG GAG	240
	Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu	
	65 70 75 80	
30	GAC GTG AAT AGC CGC AGG GAC ATC CTG CCG GAC TAT GAG CTC AAG CTC	288
	Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu	
	85 90 95	
35	ATC CAC CAC GAC AGC AAG TGT GAT CCA GGC CAA GCC ACC AAG TAC CTA	336
	Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu	
	100 105 110	
40	TAT GAG CTG CTC TAC AAC GAC CCT ATC AAG ATC ATC CTT ATG CCT GGC	384
	Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly	
	115 120 125	
45	TGC AGC TCT GTC TCC ACG CTG GTG GCT GAG GCT GCT AGG ATG TGG AAC	432
	Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn	
	130 135 140	
50	CTC ATT GTG CTT TCC TAT GGC TCC AGC TCA CCA GCC CTG TCA AAC CGG	480
	Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg	

	145	150	155	160	
	CAG CGT TTC CCC ACT TTC TTC CGA ACG CAC CCA TCA GCC ACA CTC CAC				528
	Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His				
5		165	170	175	
	AAC CCT ACC CGC GTG AAA CTC TTT GAA AAG TGG GGC TGG AAG AAG ATT				576
	Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile				
		180	185	190	
10	GCT ACC ATC CAG CAG ACC ACT GAG GTC TTC ACT TCG ACT CTG GAC GAC				624
	Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp				
		195	200	205	
15	CTG GAG GAA CGA GTG AAG GAG GCT GGA ATT GAG ATT ACT TTC CGC CAG				672
	Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln				
		210	215	220	
	AGT TTC TTC TCA GAT CCA GCT GTG CCC GTC AAA AAC CTG AAG CGC CAG				720
20	Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln				
		225	230	235	240
	GAT GCC CGA ATC ATC GTG GGA CTT TTC TAT GAG ACT GAA GCC CGG AAA				768
	Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys				
25		245	250	255	
	GTT TTT TGT GAG GTG TAC AAG GAG CGT CTC TTT GGG AAG AAG TAC GTC				816
	Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val				
		260	265	270	
30	TGG TTC CTC ATT GGG TGG TAT GCT GAC AAT TGG TTC AAG ATC TAC GAC				864
	Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp				
		275	280	285	
35	CCT TCT ATC AAC TGC ACA GTG GAT GAG ATG ACT GAG GCG GTG GAG GGC				912
	Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly				
		290	295	300	
	CAC ATC ACA ACT GAG ATT GTC ATG CTG AAT CCT GCC AAT ACC CGC AGC				960
40	His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser				
		305	310	315	320
	ATT TCC AAC ATG ACA TCC CAG GAA TTT GTG GAG AAA CTA ACC AAG CGA				1008

	Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	Phe	Val	Glu	Lys	Leu	Thr	Lys	Arg	
					325					330					335		
	CTG	AAA	AGA	CAC	CCT	GAG	GAG	ACA	GGA	GGC	TTC	CAG	GAG	GCA	CCG	CTG	1056
5	Leu	Lys	Arg	His	Pro	Glu	Glu	Thr	Gly	Gly	Phe	Gln	Glu	Ala	Pro	Leu	
				340					345					350			
	GCC	TAT	GAT	GCC	ATC	TGG	GCC	TTG	GCA	CTG	GCC	CTG	AAC	AAG	ACA	TCT	1104
10	Ala	Tyr	Asp	Ala	Ile	Trp	Ala	Leu	Ala	Leu	Ala	Leu	Asn	Lys	Thr	Ser	
			355				360					365					
	GGA	GGA	GGC	GGC	CGT	TCT	GGT	GTG	CGC	CTG	GAG	GAC	TTC	AAC	TAC	AAC	1152
	Gly	Gly	Gly	Gly	Arg	Ser	Gly	Val	Arg	Leu	Glu	Asp	Phe	Asn	Tyr	Asn	
			370				375					380					
15	AAC	CAG	ACC	ATT	ACC	GAC	CAA	ATC	TAC	CGG	GCA	ATG	AAC	TCT	TCG	TCC	1200
	Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	Arg	Ala	Met	Asn	Ser	Ser	Ser	
			385				390				395				400		
20	TTT	GAG	GGT	GTC	TCT	GGC	CAT	GTG	GTG	TTT	GAT	GCC	AGC	GGC	TCT	CGG	1248
	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp	Ala	Ser	Gly	Ser	Arg	
				405						410					415		
	ATG	GCA	TGG	ACG	CTT	ATC	GAG	CAG	CTT	CAG	GGT	GGC	AGC	TAC	AAG	AAG	1296
25	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	Gln	Gly	Gly	Ser	Tyr	Lys	Lys	
				420					425					430			
	ATT	GGC	TAC	TAT	GAC	AGC	ACC	AAG	GAT	GAT	CTT	TCC	TGG	TCC	AAA	ACA	1344
30	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	Asp	Leu	Ser	Trp	Ser	Lys	Thr	
			435						440					445			
	GAT	AAA	TGG	ATT	GTT	ATA	TCC	AGA	ACT	CAC	AGC	CCA	ACC	TGA			1386
	Asp	Lys	Trp	Ile	Val	Ile	Ser	Arg	Thr	His	Ser	Pro	Thr	*			
			450					455					460				
35																	

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 461 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

Met Gly Pro Gly Ala Pro Phe Ala Arg Val Gly Trp Pro Leu Pro Leu
5      1              5              10              15

Leu Val Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser
              20              25              30

10  Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser Ser
              35              40              45

Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly
              50              55              60

15  Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu
              65              70              75              80

Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu
20              85              90              95

Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu
              100             105             110

25  Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly
              115             120             125

Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn
              130             135             140

30  Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg
              145             150             155             160

Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His
35              165             170             175

Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile
              180             185             190

40  Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp
              195             200             205

Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln

```

	210	215	220
	Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln		
	225	230	235 240
5	Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys		
	245	250	255
	Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val		
10	260	265	270
	Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp		
	275	280	285
15	Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly		
	290	295	300
	His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser		
	305	310	315 320
20	Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg		
	325	330	335
	Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu		
25	340	345	350
	Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser		
	355	360	365
30	Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn		
	370	375	380
	Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser		
	385	390	395 400
35	Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg		
	405	410	415
	Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys		
40	420	425	430
	Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr		
	435	440	445

Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser Pro Thr
 450 455 460

5

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1746 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: cDNA to mRNA

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Canis familiaris

(ix) FEATURE:

25

(A) NAME/KEY: CDS

(B) LOCATION:1..1746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

30	ATG CTG CTG CTG CTC CTG CCG CTG GCG CTG GCG CCG CTC TTC CTC CGC	48
	Met Leu Leu Leu Leu Leu Pro Leu Ala Leu Ala Pro Leu Phe Leu Arg	
	1 5 10 15	
35	CCC CCG GGC GCG GGC GGG GCA CAG ACC CCC AAC GCC ACC TCG GAA GGT	96
	Pro Pro Gly Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly	
	20 25 30	
40	TGC CAG ATC ATA CAC CCG CCT TGG GAA GGG GGT ATC AGG TAC AGG GGC	144
	Cys Gln Ile Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly	
	35 40 45	
	CTG ACT CGT GAC CAG GTG AAG GCT ATC AAC TTC CTG CCG GTG GAC TAT	192
	Leu Thr Arg Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr	
	50 55 60	

	GAG ATT GAG TAT GTG TGC CGG GGA GAG CGA GAG GTG GTG GGG CCC AAG	240
	Glu Ile Glu Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys	
	65 70 75 80	
5	GTC CGA AAG TGC CTG GCC AAT GGC TCC TGG ACA GAT ATG GAC ACA CCC	288
	Val Arg Lys Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro	
	85 90 95	
10	AGC CGC TGT GTC CGA ATC TGT TCC AAG TCA TAT TTG GCC CTG GAA AAT	336
	Ser Arg Cys Val Arg Ile Cys Ser Lys Ser Tyr Leu Ala Leu Glu Asn	
	100 105 110	
	GGG AAG GTC TTC CTG ACG GGT GGG GAC CTC CCC GCT CTG GAT GGA GCC	384
15	Gly Lys Val Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala	
	115 120 125	
	CGG GTG GAT TTC CGG TGT GAC CCT GAC TTC CAT CTT GTG GGC AGC TCC	432
	Arg Val Asp Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser	
20	130 135 140	
	CGG AGT ATC TGT AGT CAG GGC CAG TGG AGC ACT CCC AAG CCC CAC TGC	480
	Arg Ser Ile Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys	
	145 150 155 160	
25	CAG GTG AGC CGA ACG CCG CAC TCA GAG CGG CGA GCG GTG TAC ATC GGG	528
	Gln Val Ser Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly	
	165 170 175	
30	GCG CTG TTT CCC ATG AGC GGG GGC TGG CCG GGG GGC CAG GCC TGC CAG	576
	Ala Leu Phe Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln	
	180 185 190	
	CCC GCG GTG GAG ATG GCG CTG GAG GAC GTG AAT AGC CGC AGG GAC ATC	624
35	Pro Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile	
	195 200 205	
	CTG CCG GAC TAC GAG CTC AAG CTC ATC CAC CAC GAC AGC AAG TGT GAC	672
	Leu Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp	
40	210 215 220	
	CCA GGC CAA GCT ACC AAG TAC CTG TAT GAA CTG CTC TAC AAC GAC CCC	720
	Pro Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro	

	225	230	235	240	
	ATC AAG ATC ATC CTC ATG CCT GGC TGC AGC TCT GTC TCC ACG CTT GTG				768
	Ile Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val				
5		245	250	255	
	GCT GAG GCT GCC AGG ATG TGG AAC CTC ATT GTG CTC TCC TAT GGT TCC				816
	Ala Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser				
		260	265	270	
10	AGC TCA CCA GCT CTG TCC AAC CGG CAG CGC TTT CCT ACC TTC TTC CGA				864
	Ser Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg				
		275	280	285	
15	ACT CAT CCC TCG GCC ACG CTC CAC AAC CCT ACG CGA GTG AAG CTC TTT				912
	Thr His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe				
		290	295	300	
	GAG AAG TGG GGC TGG AGG AAG ATT GCC ACC ATC CAG CAG ACC ACC GAG				960
20	Glu Lys Trp Gly Trp Arg Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu				
		305	310	315	320
	GTG TTC ACA TCG ACT CTG GAC GAC CTA GAG GAA CGA GTG AAG GAG GCT				1008
	Val Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala				
25		325	330	335	
	GGG ATT GAG ATT ACT TTC CGC CAG AGC TTC TTC TCA GAT CCT GCC GTG				1056
	Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val				
		340	345	350	
30	CCT GTC AAG AAC CTC AAG CGC CAG GAT GCC CGA ATC ATC GTG GGA CTT				1104
	Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu				
		355	360	365	
35	TTC TAT GAG ACT GAA GCC CGG AAA GTG TTC TGT GAG GTA TAC AAG GAG				1152
	Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu				
		370	375	380	
	CGG CTC TTT GGG AAG AAG TAT GTG TGG TTC CTC ATT GGG TGG TAT GCT				1200
40	Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala				
		385	390	395	400
	GAC AAT TGG TTC AAG ACC TAC GAC CCC TCC ATC AAC TGC ACA GTG GAT				1248

	Asp	Asn	Trp	Phe	Lys	Thr	Tyr	Asp	Pro	Ser	Ile	Asn	Cys	Thr	Val	Asp	
					405					410					415		
	GAG	ATG	ACC	GAG	GCT	GTG	GAA	GGC	CAC	ATC	ACC	ACT	GAG	ATT	GTC	ATG	1296
5	Glu	Met	Thr	Glu	Ala	Val	Glu	Gly	His	Ile	Thr	Thr	Glu	Ile	Val	Met	
					420				425					430			
	CTG	AAC	CCA	GCC	AAC	ACC	CGC	AGC	ATC	TCC	AAC	ATG	ACA	TCC	CAG	GAG	1344
10	Leu	Asn	Pro	Ala	Asn	Thr	Arg	Ser	Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	
			435					440				445					
	TTT	GTG	GAG	AAA	CTG	ACC	AAG	AGA	CTC	AAG	AGA	CAC	CCT	GAG	GAG	ACA	1392
	Phe	Val	Glu	Lys	Leu	Thr	Lys	Arg	Leu	Lys	Arg	His	Pro	Glu	Glu	Thr	
			450				455					460					
15																	
	GGC	GGC	TTC	CAG	GAG	GCA	CCG	CTG	GCC	TAT	GAT	GCC	ATC	TGG	GCC	TTG	1440
	Gly	Gly	Phe	Gln	Glu	Ala	Pro	Leu	Ala	Tyr	Asp	Ala	Ile	Trp	Ala	Leu	
	465					470					475				480		
20	GCA	TTG	GCC	CTG	AAC	AAG	ACA	TCT	GGA	GGG	AGC	GGC	CGT	TCG	GGG	GTG	1488
	Ala	Leu	Ala	Leu	Asn	Lys	Thr	Ser	Gly	Gly	Ser	Gly	Arg	Ser	Gly	Val	
					485				490					495			
	CGC	CTG	GAA	GAC	TTC	AAC	TAC	AAC	AAC	CAG	ACG	ATC	ACA	GAC	CAA	ATC	1536
25	Arg	Leu	Glu	Asp	Phe	Asn	Tyr	Asn	Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	
				500					505					510			
	TAC	CGC	GCA	ATG	AAC	TCC	TCG	TCC	TTT	GAG	GGT	GTC	TCT	GGC	CAC	GTG	1584
30	Tyr	Arg	Ala	Met	Asn	Ser	Ser	Ser	Phe	Glu	Gly	Val	Ser	Gly	His	Val	
			515					520					525				
	GTG	TTT	GAT	GCC	AGC	GGC	TCA	CGG	ATG	GCC	TGG	ACT	CTG	ATT	GAG	CAG	1632
	Val	Phe	Asp	Ala	Ser	Gly	Ser	Arg	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	
			530				535					540					
35																	
	CTG	CAG	GGT	GGC	AGC	TAC	AAG	AAG	ATC	GGC	TAC	TAT	GAC	AGC	ACC	AAG	1680
	Leu	Gln	Gly	Gly	Ser	Tyr	Lys	Lys	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	
	545					550					555				560		
40	GAT	GAC	CTT	TCC	TGG	TCT	AAA	ACG	GAC	AAA	TGG	ATT	GTT	ACA	TCC	AGA	1728
	Asp	Asp	Leu	Ser	Trp	Ser	Lys	Thr	Asp	Lys	Trp	Ile	Val	Thr	Ser	Arg	
					565					570					575		

ACT CCC AGC CCA ACT TGA

1746

Thr Pro Ser Pro Thr *

580

5

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 581 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Met Leu Leu Leu Leu Leu Pro Leu Ala Leu Ala Pro Leu Phe Leu Arg

1

5

10

15

20

Pro Pro Gly Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly

20

25

30

Cys Gln Ile Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly

25

35

40

45

Leu Thr Arg Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr

50

55

60

30

Glu Ile Glu Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys

65

70

75

80

Val Arg Lys Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro

85

90

95

35

Ser Arg Cys Val Arg Ile Cys Ser Lys Ser Tyr Leu Ala Leu Glu Asn

100

105

110

Gly Lys Val Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala

40

115

120

125

Arg Val Asp Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser

130

135

140

HI865-1 WO SEQ

85

Arg Ser Ile Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys
 145 150 155 160

5 Gln Val Ser Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly
 165 170 175

Ala Leu Phe Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln
 180 185 190

10 Pro Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile
 195 200 205

Leu Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp
 15 210 215 220

Pro Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro
 225 230 235 240

20 Ile Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val
 245 250 255

Ala Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser
 260 265 270

25 Ser Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg
 275 280 285

Thr His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe
 30 290 295 300

Glu Lys Trp Gly Trp Arg Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu
 305 310 315 320

35 Val Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala
 325 330 335

Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val
 340 345 350

40 Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu
 355 360 365

	Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu	
	370	380
	Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala	
5	385	390 395 400
	Asp Asn Trp Phe Lys Thr Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp	
	405	410 415
10	Glu Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met	
	420	425 430
	Leu Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu	
	435	440 445
15	Phe Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr	
	450	455 460
	Gly Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu	
20	465	470 475 480
	Ala Leu Ala Leu Asn Lys Thr Ser Gly Gly Ser Gly Arg Ser Gly Val	
	485	490 495
25	Arg Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile	
	500	505 510
	Tyr Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val	
	515	520 525
30	Val Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln	
	530	535 540
	Leu Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys	
35	545	550 555 560
	Asp Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Val Thr Ser Arg	
	565	570 575
40	Thr Pro Ser Pro Thr	
	580	

((2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 3415..3440

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 3441..3903

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 3904..3988

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 3989..4689

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 4690..4893

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 4894..5645

(ix) FEATURE:

- (A) NAME/KEY: exon

(B) LOCATION:5646..5831

(ix) FEATURE:

(A) NAME/KEY: intron

5 (B) LOCATION:5832..7181

(ix) FEATURE:

(A) NAME/KEY: exon

10 (B) LOCATION:7182..7202

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:7203..8307

15 (ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:8308..8803

(ix) FEATURE:

20 (A) NAME/KEY: intron

(B) LOCATION:8804..12266

(ix) FEATURE:

(A) NAME/KEY: exon

25 (B) LOCATION:12267..12401

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:12402..12815

30

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:12816..12986

35 (ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:12987..14085

(ix) FEATURE:

40 (A) NAME/KEY: exon

(B) LOCATION:14086..14187

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:14188..14473

(ix) FEATURE:

5 (A) NAME/KEY: exon

(B) LOCATION:14474..14539

(ix) FEATURE:

10 (A) NAME/KEY: intron

(B) LOCATION:14540..14998

(ix) FEATURE:

15 (A) NAME/KEY: exon

(B) LOCATION:14999..15190

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:15191..16862

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

	GATCATATTA ATTTGAAGGT GCGGGGGCAG GATGGTTCTG TGGTGCAGTT TAAGATTAAG	60
25	AGGCATACAC CACTTAGTAA ACTAATGAAA GCCTATTGTG AACGACAGGG ATTGTCAATG	120
	AGGCAGATCA GATTCCGATT CGACGGGCAA CCAATGAAAC AGACACACCT GCACAGTTGG	180
	AAATGGAGGA TGAAGATACA ATTGATGTGT TCCAACAGCA GACGGGAGGT GTCTACTGAA	240
30	AAGGGAACCT GCTTCTTTAC TCCAGAACTC TGTTCTTTAA AGACCAAGAT TACATTCTCA	300
	ATTAGAAAAC TGCAATTTGC TTCCACCACA TCCTGACTAC TACCGTATAG TTTTCTCTAT	360
35	TCTTTCATTT CCCCCTTCCC CATTCCTTTA CTGTACATAA AGTAACTGGT ATATGTGCAC	420
	AAGCATATTA CTTTTTTTTT TTAAACTAA ACAGCCAATG GTATGTTTTG ATTGACATCA	480
	AGTGGAGACG GGGGGGAAAA TACTGATTCT GTGAAAATAC CCCCTTTCTC CATTAGTGGC	540
40	ATGCTCATTC AGCTCTTATC TTTATATTCC AGTAAGTTAT TTTGCTCTCA CTGTTTTAAC	600
	AACAACAACA AAAAAACAAC AACATAAAAA TCCTTGCATA CCTTGTTCAA TTGGAGAATT	660

	TTAATGTTTT TCATTTATCA TTGTAAAACC AAGGACAATT TTATAACTTT TTTGTACTTA	720
	GCTGTACAT GCAGAGCAAT CTGTCTTTAA GTAGGGATAA ATTACTCTAA AACAAAAAAG	780
5	AATCCTAGAT AGTTTTCCCT TCAAGTCAAG CGTCTTGTTG TTTAAATAAA CTTCTTGTTT	840
	AAAAAAAAAA AAAGTAAAAA AGAAAAGTTA TGCAACAATT AATGGCCCAG AGGCAATCCT	900
10	TGTTAACATT TTGATGCATC TTTTAGCTGT TTTTTTTTTT TTTTTTTTTT TTGACTGAGT	960
	TTGACTCTTG TCACCCAGGC TGAAGTGCAA TGGCATGGCA TGATCTTGGC TCACTGCAAC	1020
	CTCCGCCTCC CGGGTTCAAG TGATTCTCCT GCCTCAGCCT CCTGAGTAGC TAGGATTACG	1080
15	GGCATGCACC ACCATGCCTG GCTAATTTTG TATTTTTAGT AGAGTTGGGG CTTCTCCACA	1140
	CTGGTCAGGC TGGTCTCGAA CTCCCAACCT CAGGTGATAA GGAAGGGGC ACTATTGACA	1200
20	TTTATGGTTG GGGCAGAGGT GTAAGATATT CTTCAAAGCA CTACCTACAT GTTGAAGAAT	1260
	TGTTCCCTCAC CCAGATTCTC AAAAGTCCCC CAGGACATTC ACGTAGTGAA AACCTGTGTT	1320
	TAATTATCTG AGCCTATAAC TTAATACAGT TTTAAAATTT TTTTTTAAAT ATACAGTGAA	1380
25	CTTTCTAGGA ATGCAATTAT AGTTGTGTGT AAAATTAGGG AAAATTAACT TTGCTACCAA	1440
	GAGTTGTTCA ACATTTTGTT AAATCACTTC ATTGATGGCA ACATGCTGGA GGTAGTTGAG	1500
30	TCACCAACTC AGCACCTGGA TCAGCCTGTG TTGGTAGCAG TTTCATCCCC GTGGTTCTGT	1560
	GAATAGGTGG AAGCATCTGC TTACTCCATC AGGACTTCTA GGGTAGTCGG GCCTTGGCAC	1620
	TCACACATTA AAATACTGTT TATGTTATTT TATTGCAAGT TACTTTTCTT TCATTTCCCC	1680
35	TTTACGTTAC AGAAAGGGAA GCATTTTGCT TTCTGTTTAA AGTTGTGTAT GTAGGTAGGT	1740
	TATATCATCT AWGACTTTCT CTCCCTCCTT CCCTTTCTTT TTGTTTGAGA TGGAGTCTTG	1800
40	CTCTGTCACC CAGGCTGGAG TGCAGTGGTG CGATCTTGGC TCACTGCAAC CTCTGCCTCC	1860
	CGGGTTCAAG CGATTCTGGT GTCTCAGCTG GGATTACAGG CGCACACCAT CACACCACGC	1920

	TAATTTTCT ATTTTAGTA GAGATGGGGT TTCGCCATGC TGGCCAGGCC AGGCTGGTCT	1980
	CAAACCTCTG AGCTCAAGTG ATCAGTCCGC CTCGGCCTCC CAAAGTTCTG GGATTTTCAGG	2040
5	CGTGAGCCTC ATCTATGAAT CTCAATTTAG GACAGTAAAA GTGTCATTAC AAAAATATTT	2100
	ATTGTAAAAA AGGGTTGGAG GTTGAGAATC TCAATTCTAG TCAGTCTCTC AGTGTTTGGT	2160
	TTCTTCCTAC CATTTTTCCT CCTAGGACCA GCCAGAAAGC AGCTTTTTTTT TTGTCCCCCT	2220
10	CAACAAGGAG CCCACTGTTT CCTCTCCCAG CCCAACTCA GGCCTACGAA CAACAACAGC	2280
	ACTACACACA CACACACACA CACACACACA CACACACACA CCCCCCTCCA CTTCAAGGTA	2340
15	TAGCCAAGAG CTTCTGGAGC CGTCAAAAAG GTCTGTACCT GCTGTCTTTA GAGCTTCCAG	2400
	TTTGCCCTTG GTCAAGAAAT ACTGTTTGCT AGGCTCTGCT GGAGTACATC AGGTAATACT	2460
	GGCTTCTAAA CCACCCTGAG GTTCTTTTCT CTTGTCTTTT TACTCCCTTC GACTTCAAT	2520
20	TTCTCTCCTT GATGTCCCCC TCCCTGTTTT GTTTTTTGCC TCCAATCCGT TCTGCGCGTT	2580
	CCCTGCAGAG CAGGCGAGTA GCAATGCTGC TGGACCATGG AGCTGCTCTA GTCTCCCAGA	2640
25	AATCTCTTCT ACACCCAACC CTTCTTGCGC TTAGGTGGTC CTCAGTCCCC CTCCCCCACC	2700
	TCCTTCTGAC CCAGGCTTCT TTCTCGCCCT CCGGTGCGAG TTCTCCTGGG CATCTGCCTC	2760
	TGCCTCTCTC CTCTCACCCG GATCTAGGGC TGCCTTCTCT TTGTGCAGCC GTCTTTCTCC	2820
30	ACCTTCATCC CAGACTCCCT GTCTCAGCGC CAGCTCCTCT GCCTTTGGCT CGGGTTCCCT	2880
	CTCCCCCACC CCAGCTTCCA GTTGTTTGGC CCGCAGGTCC CTCGGCAGTG ACCGGCGCCC	2940
35	CCCGACGAGT GCGTGTGCAC CAGGGCACCT CCCTCTCCCC CACCTCTCAG CCCCGCGCCT	3000
	CTCCACCGCC CGCCCCACCG CGCTGTGGGC GGTCCAGGGC GGGGCTGGGA TCCGGGGCGG	3060
	CTCCCGGGGC TCGGGTTGTG GGAGGCGCCC TCTCCCCGGT CTTCCCCTCT CTTCCCCCG	3120
40	CCCTGCCTTC CTTGACCC TCCTTCTTCC CTCCGCCCCG GAGCTCTCCC TGGTCCCCGG	3180
	CGCCGCTCC TTCCCTCCCG GCTCCCCGCT CCCCCTCCC GTGGCTGCCG CCGCCCCGGG	3240

	GAAGAAGAGA CAGGGGTGGG GTTTGGGGGA AGCGAGAGAG GAGGGGAGAG ACCCTGGCCA	3300
	GGCTGGAGCC TGGATTCGAG GGGAGGAGGG ACGGGAGGAG GAGAAAGGTG GAGGAGAAGG	3360
5	GAGGGGGGAG CGGGGAGGAG CGGCCGGGCC TGGGGCCTTG AGGCCCCGGG AGAGCCGGGG	3420
	AGCCGGGCCC GCGCGCCGAG GTAAGAGCCA GGGCCCCGGG TTAGCAGGGC TCGGAGAGGG	3480
10	GGCGCGCGGC GTGGTGGGGG AGGGGGCAGT GGGCGCAGGG CCCAGCTGGG GGAAGCGGGG	3540
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	GAGCGTGGGT AAGCCAGGCT TCTGCGAGCC GCGGGGGCCG GGGGAGAGGA GGTGGTGAGA	3660
15	GGTGGAGTCC GGGAGGGTTG GGGGCCGAGG GAGGCAGGAG GAGGGTGGGG ACAGGCTTTC	3720
	TCTCCTCCTC TCCCCCACC CCGCGCGGGG CTCCGCCCCC GCCTCCTCCG CGGGGCGCTC	3780
20	TCTTGGTCCC CAGGCTGAGC CCGGTCGGAG CCTGCGAGGC AACC GGCAAG AGGTCGAGTA	3840
	GTCTCCGGGT GCGGGCCGCG CCGGCGGGGC TCGGTCCAGT CCTCATGGCC GCCTCTCACT	3900
	TAGATGTTGC TGCTGCTGCT ACTGGCGCCA CTCTTCCTCC GCCCCCGGG CGCGGGCGGG	3960
25	GCGCAGACCC CCAACGCCAC CTCAGAAGGT GCATCCTTCT TCGACGACCT CCGGCCCTCC	4020
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30	GTCCACATA TCATCCCGGT CTGGCAACCC CTTCTGCTCG GCCCGACTTT ACTACTGCTG	4140
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	ACTATACCAC CTTCTGTGCT ATTTTCTCCG CCTCAATCCC CTTTCCCAGC CCCACATTAC	4260
35	TACCTCAATT ACTCCCTTTT CTTGGTCCCA CTTTGCTGTC CAGATGATCT TATTAGCCTC	4320
	CCTTTATCCT CCTATCCTAA TTCAACTGGA ATATCCTCAT TTAGCCTTTT TTTTAAAGA	4380
40	AAAGCTCCAC CCACATATCA TACCCTTCAT GATTTCTTAA TTACTTTTCT TTCTTACCTC	4440
	CACCCAGCAC CCTTCCCTCC CCACTTGTGG GTTCTCTCAT CAGCTTTAAC CCTGGCCCTT	4500

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	CATCCCTCTT	CCTCTGTCCC	CAGCCTGCCC	ACAGACCACG	CCCTACTCTC	CCCTTCCTCC	4620
5	CACTGGGGAG	CCTGCCTTTT	CCTCTTTCCC	ACCATTCCCTC	TCTGTATGCC	TCCCCGACTC	4680
	ACCCCTTAGG	TTGCCAGATC	ATACACCCGC	CCTGGGAAGG	GGGCATCAGG	TACCGGGGCC	4740
	TGACTCGGGA	CCAGGTGAAG	GCTATCAACT	TCCTGCCAGT	GGACTATGAG	ATTGAGTATG	4800
10	TGTGCCGGGG	GGAGCGCGAG	GTGGTGGGGC	CCAAGGTCCG	CAAGTGCCTG	GCCAACGGCT	4860
	CCTGGACAGA	TATGGACACA	CCCAGCCGCT	GTGGTGAGTA	GCCTCGGAAG	CCCCTCCCCT	4920
15	CTTCAAGACT	ATTCCTTTTT	CTGCCGCAA	CTTAGCATT	CTGCTTGCAA	GTCAGCACTT	4980
	TAAATCCAGT	ATACCAAAT	TCACAAATAC	ATTTATTGAA	TGACTACTAC	ATAAGAGCAA	5040
	TTTTGCTCTG	TGCGGTGGA	GGTAGTAGAG	CTAGCAGCCT	GCACAGTTCA	TTTCATCCTC	5100
20	CCTTCATTAG	GCCACTGATC	ATTGGCCTAT	AACATTGATA	ATTCATCTTG	TCAGTTATTC	5160
	TCTTTGAGGA	TCATTAGTGG	CAGATGATGA	CAAAAAATT	CTAAAATGAT	TTCATCACAT	5220
25	TTTTGAATAC	CTCTGTCACC	AACCCAGAGA	CCATATGCCC	AAGAAACAAA	AGCCAGTTTA	5280
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30	ATTTTGTGTG	CTTATAGCCC	CATCTTGGGT	TCCTAAAATG	GTAATTTTTT	TTTTCTTTTG	5460
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	TGCTCTTTAA	AGGGAAAGAG	CCTTCTTCAA	CTCGCCTCTC	TTCTTATTTT	CCTATCTCTC	5640
	CACAGTCCGA	ATCTGCTCCA	AGTCTTATTT	GACCCTGGAA	AATGGGAAGG	TTTTCTTGAC	5700
40	GGGTGGGGAC	CTCCCAGCTC	TGGACGGAGC	CCGGGTGGAT	TTCCGGTGTG	ACCCCGACTT	5760
	CCATCTGGTG	GGCAGCTCCC	GGAGCATCTG	TAGTCAGGGC	CAGTGGAGCA	CCCCAAGCC	5820

	CCACTGCCAG	GGTGAGGGGA	ACAGCTGCCT	GCATGCAGCT	GATGAGGACG	CTTGTGTGAG	5880
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5	AGGACACTGG	AAAGGGGAGA	TGAAAGTCCC	TTTTTCCTCC	ATCACCTGCC	TCAAACCTCC	6000
	TCTTGCAGTC	CCCGGTATCC	TCTGTAGGTT	GGGGGCTTCC	TTCCTTTACC	TTTTAAAAAA	6060
10	ATCTTCCTGC	TCCCGATTCT	TAGACCTCAC	GTTTTCTCTT	TTCCTTTATG	AATCTCACCT	6120
	CTCTCACCTT	CTTCAGGTTT	AAATACTCCA	ATTTTCCCTT	TCTCTAAACT	TAGAAATTTT	6180
	CATGCATCAC	CCTCTTCTAG	AATTCATCCC	TCACCATTCC	TTATATAATT	GATTTATTGT	6240
15	AAAGACTCAG	AAATAAATCA	AACATTCTAC	TAAGAAAAAT	TGAGAAGGGG	AGCTCTGGGG	6300
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20	ACAACTCAGG	GATGGGGTGG	GAAGAAGACA	GGTCCTTTTC	TGKACTTCCT	AGACAACCTC	6420
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25	GGATGCAGTC	ATCCCATTTG	TATGCCTCAT	ACTTCCTCTA	CCCTGGTAGA	TTCTTTCAAG	6600
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30	TTCTGGAAAT	TGAGAGTCCC	ATCCAGGGGT	GGACTTATGA	CAC'TACTGAA	ACTTAGACTT	6720
	CAAGGTTCCCT	CACCTACAGG	GCCCTCTTCC	TGTGCTCTAA	TAATATAGAG	GGCTCGATGG	6780
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35	ATTGCTTAAA	GCCAATTGTA	TGTGTAATTT	TTTTTCTTAA	AGACTCCCAA	TTTTGTAATA	6900
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40	TTCTGTTGTC	CTATGAAAAA	TCGAAGAAGA	AAATAAGTCC	TGACCCCTT	ACCCCCAGAC	7020
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5	AGGTGAGATG	AGAAACCCCT	ACCGCGCGCA	CTGCAATGCC	CTCCCCCTTCA	CTCTGCACCC	7260
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10	GTTTTCACG	AGGCTGCGGT	CTCTCCTTGT	CCCTGCTTGG	CTACACTTCC	CTGGGCTCCA	7440
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	GAACCTTTTC	CAGCCTGCTG	CCTCCTAGGA	TTTCACCTAA	TGGACTTTCT	CAGCCTGTCC	7620
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25	ACCCAACCTCG	TTCCCTCCAA	AACCGTTTCC	TCTCCCCCAC	ATCCTCAGTG	CTTCACTGTA	7860
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35	CCGCCCCCTCC	GACTGTGCT	CCCACCTCGG	CGCTCGCTTC	CCTCCCCGCC	CCCTTCCTGC	8160
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5	CCGGGTGGGG	TGGCCACTGC	CGCTTCTGGT	TGTGATGGCG	GCAGGGGTGG	CTCCGGTGTG	8580
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10	AGAACGGGCG	GCAGTGTA	TCGGGGCACT	GTTTCCCATG	AGCGGGGGCT	GGCCAGGGGG	8700
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40	GAGAACAGAA	AAGAATGGCA	GTGGGGGAGA	GGGGCAAGGA	GGTAGCGTGG	GGATAATGAG	9600
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35	GGTATGTTCA	TTAATACCAA	AGGAGGGGTG	TGCAGGAGAG	GTGATGGGTA	AGGCTCCAGA	12060
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40	TGCCAGAAAG	GAGAAGAAAA	CGGTAATTAA	TGATGAAAGT	GAGTAATTGA	GAAAGGAACT	12180
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5	CGCTGGTGGC TGAGGCTGCT AGGATGTGGA ACCTCATTTGT GGTAAGCAGG GCTATGGGGG	12420
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	GAGAGGAAAT	ACAGGCTCTA	CATCTGAAGA	AGGCAGTCTG	CTCCCTCCCT	TTTATTCTAT	13620
	TCTTTGGGTC	TTCTATCCAC	TGTGTTTCA	GGCCCTTTAA	TCCTCCCCCA	CTTTCACTCT	13680
5	GATTCAGACC	ATTCTTCTCT	GATCCTTTGT	CTGTCTGCCC	ATTTGCCTCT	TGAGGTTGAC	13740
	ATCATGCTGT	CTGTCCCAGT	CCTTGCCCTG	TCTTTTCCTG	GTTCCCTTTAT	GTTTCTTTAC	13800
10	CCCATCTTTG	CCTTCAGTGG	TAGGAGTGGG	TGAATGGAGT	GGCTTCCCCC	ACACAGAGCC	13860
	TCAGCAGGGG	CTCACCATT	ACCTTCCCAC	TTGGAATCCA	CATCCTAAGA	CCAGATGCCT	13920
	TCCCGAACTC	CTCACTTCAG	GGACAGAAGC	TGTTGAAGGA	AGGTTCAGAA	TGGCTGCTTC	13980
15	TTTGCTCTAT	CTGAGTATTG	CTCTGAAATC	CCCAGTTAAC	CTCTCTGGTC	TTTATTCCCT	14040
	CATGCACCCC	GTGTTTTTCC	AACTTGTTTT	TTATTCCCAC	CCAAGACTCT	GGACGACCTG	14100
20	GAGGAACGAG	TGAAGGAGGC	TGGAATTGAG	ATTACTTTCC	GCCAGAGTTT	CTTCTCAGAT	14160
	CCAGCTGTGC	CCGTCAAAAA	CCTGAAGGTC	AGATGGCTGG	GAGTGGTGGG	CTCTGTTTAC	14220
	GGAGGGACCA	AGCTGGGGGA	CAGTGACTGG	TTGGAGAGGA	AAGCCAGGCG	GGGGCAGGTT	14280
25	TTGATTCTCT	GAGGCAATAG	CATCTCCTGG	GGAAGTTTAG	CTCCATCTTC	CAGTTGACGT	14340
	TTATTCACTA	TACGTTGAGC	GTTACCCTGC	ACTAAGCACT	TTGGGATGGG	AAATCAAAGC	14400
30	TGTGAAGACA	TCTGGCTTAG	CCCCTCAGGC	ATTCCCGGGC	ATCCCTCAGG	AGCTGTTTCT	14460
	TTCTCTGTTG	TAGCGCCAGG	ATGCCCGAAT	CATCGTGGA	CTTTTCTATG	AGACTGAAGC	14520
	CCGGAAAGTT	TTTTGTGAGG	TGGAGTTGGA	TCTGAAGAGG	GAGGGGCACT	GGGTGGGAGT	14580
35	TTCCCTTGGT	TTTCTTGTGG	GGCCTCCTCT	TGGCATCTGT	GCCTGAGTTG	ATAGCATATG	14640
	ATCTGAGGTG	ACGATTCATA	GGATGCTCT	GTCTGTTGGC	TCTGACTGCA	TCCCTTGTCT	14700
40	GCACACACAT	GATACTTTCT	TCAGATCTCA	TTTTTCTACT	GCTTTGTGTT	TCCTGAGAAG	14760
	CCCATGAATT	CCATCTGTCC	TGACTGGCTG	GAAAAGGCCA	CTCAGAAATA	CAGGGGCTGG	14820

	GGAGAACTT	AGAAGGAAGA	ATTGTCAGCC	TTTCCTACTA	TCCCCAAGAC	TTGTAGATTT	14880
	CTCTTTTTTAG	TTCTACTGCT	CTTCCCTGAT	TCCCAAGAGG	CTAAATAGTA	TCAAGTGAGA	14940
5	TAAGACAAAA	ACAAACAAAT	GAGCAAACAA	AAACTCAGCC	ATTCTCCTCT	GTATTCAGGT	15000
	GTACAAGGAG	CGTCTCTTTG	GGAAGAAGTA	CGTCTGGTTC	CTCATTGGGT	GGTATGCTGA	15060
	CAATTGGTTC	AAGATCTACG	ACCCTTCTAT	CAACTGCACA	GTGGATGAGA	TGACTGAGGC	15120
10	GGTGGAGGGC	CACATCACAA	CTGAGATTGT	CATGCTGAAT	CCTGCCAATA	CCCGCAGCAT	15180
	TTCCAACATG	GTGAGAGTGT	GGGGACTTGC	AGTCTGGCAC	CTGGGAGGGT	GGAGAGGACT	15240
15	GAGGGGGCCT	TGCAGGGGAA	AGGGTGGCAG	GGAGAGGGTG	CGGAATTTGG	ATATAAAGGA	15300
	GAAGAGGGGG	CTGTGCCCAC	CCTGAACTTG	TCTGCATTAT	GTTTCCTGTG	GATCCTACCT	15360
	TTGCTCTGAC	TTCCTTGGGT	AGAGAGAGAA	AAAAAAAAAA	ACGATGGAGT	TGTATGTTCA	15420
20	GTAGGTTCCCT	GATGAGTGGA	AGGGCTGTTA	CCATGGAGAC	GAGGAGCAGT	TGGTGAGAAG	15480
	TCAGGAGGAA	CCGGCATTAA	TGATAATATG	GATGCTTGTA	TACTCAAGCA	CACCTTTACA	15540
25	GGAGCACTGT	GTCTGGGCAG	AATTGCATTT	CATTTTCTTG	GTGATTTATG	TTAGTGTTTT	15600
	AGAGTTGCTT	AATATTCACT	CATGATTGAT	ATGCAATTAG	CTTGGATCCT	GTTGCTTTTT	15660
	TTAATGATTC	TTTTTTTAGA	ATTTTATGTG	GAGAAGGGGC	TTTTGAAATC	ATTTAGCCCC	15720
30	AGACAGCTGG	TTAATGACAG	ACTTGGAGCG	AGGAGGCGCA	TTCTCTGATT	TGAGAGGGCT	15780
	GGGGCAGCCC	TGCAGCTGAG	GGGCAGAAGT	GAGTGTGGGT	GTGGGCACAG	GGGAAGAGGC	15840
35	TTCTTTGTTG	CTCAGCACTA	CATTGTAAAG	AGTACAGGAA	TTTTGGGTAA	GCTCGATACG	15900
	GCCACCTATG	TGTCTGCTTA	TTACACCAAG	TGTGTACCTG	CTTTGGAGAG	CATGTTAGGG	15960
	GTGAGTTAAT	GGTTGTAAAG	CCCCAAAATA	GCTTGATTTA	AAAAGTTTTA	CTAACAGTGG	16020
40	CATTTGTGTG	GTACTTAGAT	TCATGATTTT	AGGGATTCTA	ACAGCAAAAC	TCTGATGTGG	16080
	ACTTATCTAC	ATTTTGTAGA	CCAGGAAAAT	GAGACTCAGA	GTGGTTTAAT	GACTTGTCTC	16140

AGGTCATGCA GCTACTCAGC AGTCCAGCTG GAATTGAATC CTAGTTAAAT CTGGCTCCAA 16200
ACTGCTCTGC TCATCACTTC CCATGGAAAA CCATGAAGCC TGACTAAAAA GTTTGTACTT 16260
5 TTATCTGCTA ACACTGTTTA GCTACTGGCA ATTGCTGAGC AAAGGAGAAA TAAGATTTAG 16320
GAAGTTGACT CTGGTGGTGT GTTGTGATGA AAGATCTGCT GCCACATGGA CTCTGATGAT 16380
10 ACACACTGTT TTGGGACATT CTAAATGGAC TCTATGTTTT AAGGTATGTT AGTTGAAAAA 16440
TACAATGAAA AAATTTTGGG AGATCACTTT CCTGTAGAGT ACCCAAGAGG TGAGTCATCC 16500
ATAAAACCTG GGAAAGTATT GGAAGTGGCT ACCAAAGCCA GAAAGACTTG TTGGTGCCCT 16560
15 GAGCCCAGGA CTTGCCAATC GTTGCTTCTG TCTTATAGCA GGGAGCTAGA GGAGGCTGAC 16620
AGAAAACAGG GATTGGCTG GATCTAGTGG CTCACACCTG TAGTCCCCAG CACCTTGGGA 16680
20 GGCCAAGGCA GAGGATCACT GGAGCCCAGG AGTTCAAGAC CAGCCTGGGC AATATAGTGA 16740
GACCCCCAGC TCTAAACAAA AAGAGAGAGA GAGAGAACAG AGAGATGGTT AGGGACATAG 16800
AGGGACACCT GAGCATTGGG GTGGGAAGAC TTGGAAGGTC CCTTTCTGAC TTTGTGTCTA 16860
25 GA 16862

30

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 16707 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:1..2742

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:2743..2985

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:2986..3613

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:3614..3677

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:3678..5226

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:5227..5304

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:5305..6848

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:6849..6999

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION:7000..7494

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION:7495..7627

(B) LOCATION:11370..11591

(ix) FEATURE:

(A) NAME/KEY: exon

5 (B) LOCATION:11592..11735

(ix) FEATURE:

(A) NAME/KEY: intron

10 (B) LOCATION:11736..12512

(ix) FEATURE:

(A) NAME/KEY: exon

15 (B) LOCATION:12513..13999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

AGCTAATTTT	GGAATTTTTT	TTTTTGAGAC	AGAGTTTCAT	TCTTATTGCC	CAGGCTTGAG	60
20	TGCAATGGCG	CGATCTTGGC	TCACAGCAAC	CTCCGCCTCC	CAGGTTCAAG	120
	GCCTCAGCCT	CCGGAGTAGC	TGGGATTACA	GGCATGCGCC	ACCACACCCG	180
	TATTTTTAGT	AGAGACAGGG	TTTCTCCATG	TTGCTCAGGC	TGGTCTCGAA	240
25	CAGGTGATCC	ACCCGCCTCA	GCCTCCCAA	GTGCTGGGAT	TACAGGCGTG	300
	CCCAGCTAAT	TTTTGTATTT	TTCATAGAGA	CAGGGTTTCA	CCATGTTGGC	360
30	TTGAACTCCT	GACCTCATGA	TCTGCCCGCC	TTGACCTCCC	AAAGTCCTGA	420
	GTGAGCCTCC	GTGCCCAGGC	CAAGTCTGGC	TAATTTTTAA	AAAAATTTTG	480
	TCCTCTCTGT	TTTGCCAGT	CTTGTCTCAA	ACTCCTGGGC	TCAAGGAATC	540
35	GGCCTCTGAA	AATGAAAATG	TTGGGATTAC	AGGCGTGAGC	CCCCTGTGCC	600
	TTTTTTTTTT	TTTTTTTAAA	GGCAGAGTCT	CACTCCATCG	CCCAGGCTGA	660
40	CGTGATCTCT	GCTCACTGCA	ACCTCTGCCT	CTTGAGTTCA	AGCGATTCTT	720
	TTCCCAAGTA	GCTGGGATTA	CGGGAGCCCA	CCAACACACC	CAGCTAATTT	780
				TTGTATTTTT		

	AGTAGAGACG	GGTTTCACCA	GGTTGGCCAG	GCTGTCTGGA	ATTCCCTGACC	TCAGGTGATC	840
	CACCCTCCTT	GGCCTCCCAA	AGAGCTGGGA	TTACAAGTGT	GAGCCACTGT	GCCCAGCCTG	900
5	ACTTGTTTTT	TATAATGCCT	TTTTTTTTTT	TTTTTGAGAC	GGAGTCTTGC	TCTGTCGCCC	960
	AGGCTGGAGT	GTAGTGGCGT	CATCTCAGCT	CACTGTAACC	TCCACCTCCT	GGGTTGAAGT	1020
	GATTTTCTCA	CCTCAGCCCT	CAGCCTCCTG	AGTAGTTGGG	ACTGCAAGTG	CACACCACCA	1080
10	TGCCCAGCTA	ATTTTTTGTA	TTTGTAGTAG	GATGGGGTTT	CACCATGTTG	CCCAGCTGGT	1140
	CTTTAACTCC	TGAGCTCAGG	CAGTCTGCTT	ACCTTGGCCT	CCCAAAGTGC	TAGGATTAAA	1200
15	GGTGTGAGCC	ACTGTGCCTG	GCCTTTTTTT	TTTTTTTTTT	TTTTTTGAGC	AGTTTTAGTT	1260
	TCCCAGCAGA	ATTGAGATGA	AGGTACAGAA	ACTTCCCAT	TGCTTCCCAC	ATGCATAGCC	1320
	TTCTACATTA	TCGACATCCT	CCGCCAGAGT	GGTACATTTG	TTACAACTGA	TGAACCTACA	1380
20	TTGATACATC	ATAATCACCC	AAAGTCCATA	GTTTACATTA	GAGTTCACCC	TTGGTGTTAT	1440
	ATATTCTATG	GGTTTGACCA	AATGTATAAT	GAGACGTATC	TACTATTAAA	TACTTTACAG	1500
25	AGTATTTTCA	CTGGCCTAAT	CCAATGGACA	TTTATTGTTA	CTTCATTATG	GTTGGGCACA	1560
	GTGCTAGATG	CTGATGATTA	AGAGAGGGCA	TGGGATTTGG	TCTTGTCTC	AAGGGTAGAA	1620
	CCTAGGCCCA	TTGCATCTTC	AAAGCCCAGG	CTCCTTCAAA	GCCCAGTGTA	GTAGCAACTG	1680
30	CTGTACCTTG	CCTGTGCCCT	TTGCGTATCT	CATCCTCTA	TCTCTCTAGA	AAGTTGGAGA	1740
	GAAAAGTGAG	CAAGGCATGA	GGAACAAAGT	TATTTATTTA	TTCTTCATTC	ATCTATTTAT	1800
35	TCTTTCATTA	CCGTTTGTGT	TAAAACATTC	CAAACCCAAA	CAATTATTTG	TATGGTCCCC	1860
	TGTGTATTAC	TTGTGGTTTC	CCAAGAAGTA	GTTGCTAAGC	TTTCCTTGT	ATGGTTTCTG	1920
	TGAGGTAAGG	AAGGAATGAT	GTGATTTTCT	CCAGTATGTA	GAATGCAGTT	CCAAGAGGTT	1980
40	AAGTAATTTA	CTTACAGTTA	TTTAGCCAAA	CAAGGTTACT	GCAAGGTATA	TGAAGTCAGG	2040
	TCTCTTGACC	CAGTTCATGA	GAGAGTTAAA	GGAACATATCA	TTCTTTTATAG	CTTTCATGGA	2100

	AAAAGAAGGT TGAGTGTGG GAGGGGTGTG GGTAGGATTG ATAATGGACT TCAAAAATGT	2160
	GAAGGGTATT TCTGTAGTTT TCATTCTTCT GAAAGCCTTC TAAGAGGCAG TGAACCAAAA	2220
5	GCACACAAGA ATGGCAAGAA GTTAGCATGC TGAAGAAATA TCCTCCTGGC TGGCAAGCAG	2280
	AGTGAGAAGA CTGCTATCAC CTTTTCTAGA ATCTTTTGGA ATTGTAGGAG CTGTTAGATC	2340
10	CTGGGTAAAC TCTATGAAGA AAGTCAGAAG GATCAGAGAA CATCAGTGTC ACAGCTCTTC	2400
	ATTGGAATAT CCATGTCTCC TCCTTTACTC TGCTCTACCT TCCATCCTTT GCCACTAATT	2460
	ATCCAGAGTG TTTGTCAAAA TTCTCTGTTT GCAGTCTGA GCTAGCAACT GTACACACTA	2520
15	ACACCATCAG ACACAGCTAA TACCTACTCT AGTCTAGTAG CTTCCGATCT AAGGCAGACA	2580
	CATGGGTATA GTTAAAGATT TTGAATGTAC ATGTGTCCAA TCTGACAACA GTAACACAAA	2640
20	CCATCCATTC AAGTAGAAGT GATTGAGTCA GAATTGGATT GCACCCCTTC CCCACACCC	2700
	ACACACATTT CAGTTCTTTC CTCATGATTT TTTCTCCCA AGACATCCCA GGAATTTGTG	2760
	GAGAACTAA CCAAGCGACT GAAAAGACAC CCTGAGGAGA CAGGAGGCTT CCAGGAGGCA	2820
25	CCGCTGGCCT ATGATGCCAT CTGGGCCTTG GCACTGGCCC TGAACAAGAC ATCTGGAGGA	2880
	GGCGGCCGTT CTGGTGTGCG CCTGGAGGAC TTCAACTACA ACAACCAGAC CATTACCGAC	2940
30	CAAATCTACC GGGCAATGAA CTCCTCGTCC TTTGAGGGTG TCTCTGTGAG TTAAACTTC	3000
	CTTCATACTC CCCTGTCTTC CCAATCTTGA GAGAGACTCC CAAGAGGCAC CTTCTACAAA	3060
	CATGCATTCT CTGTTTTTCT CAGTTACTTC TTTGCAGAAT CAGTCTCCGA CCAGAGAAGT	3120
35	AGGGACCTTC AAATTAGAAG AACCCATCAA AGACTAGAGG AAAAAAATG ATGTATTCCA	3180
	TTTTTTTAAA CCCCTCCCCT CATTTCTTTT CAACTAGAC CAAGTATTCA TGAGTCAGAT	3240
40	GAGAACTATA GGATTTTGAA AGACAAAACA GTCTGAAAGG TCATCTTCTT ATTCCTTTTA	3300
	AAATGAAAAG ATTAGTTTCC AGAGAGATTT GCTGACTTGC TTAGGCCACA CAACCAGAAG	3360

	CCTGCTGGTG	TTCTGTCTGG	GGATTTTTTC	CCATTCAAAT	CTCATAAGTG	AAGCTCCTTC	3420
	TCCAAAGAAT	AATGTTTCTA	AAATCTAGGG	TATGGGCATC	TGGGGTATGT	CCTATATGCA	3480
5	GGCAAATGCC	ATAAATAGCA	TTCATTGAGA	GGCTCAATTA	CATCAAAAAC	AGAAGGATTT	3540
	AAAGAGTCCC	TGATGTTCTC	TTTCACTCTT	GCTTTTGTCT	CCTTTGCCTT	GCTCCACATG	3600
	TTCTTCCCT	CAGGGCCATG	TGGTGTTTGA	TGCCAGCGGC	TCTCGGATGG	CATGGACGCT	3660
10	TATCGAGCAG	CTTCAGGGTT	AGTACAGGGG	CAGGAGGGGA	CCGGACATGG	GGGCTAGGCT	3720
	GGGGCTGGGC	TGGGATGCCC	CCTGGGGAAG	AATGCCAGAG	ACATCACAAG	ATTGCCCTGG	3780
15	CACCTCCCAA	CTTCTGCCCT	TCTCTTTTAA	CTCTGTTTAT	CAAGCTTGTA	AATAATAATA	3840
	ATAATAAGCT	TAATAACAAG	AAGATTGATG	TCTTTGAGTT	GCACTGGTTT	TGCTCTTGAA	3900
	AAGAGGTGTG	CAGGCTGGGT	GTGGTGGCTC	ACCCCTGTAA	TCCCAGCACT	TTTGGGAGGC	3960
20	CAAGGCAGGC	AGATCATGAT	CATGGTCAGG	AGTTTGAGAC	CAGCCAGACC	AACATGGTGA	4020
	AACCTGTCTC	TACCAAAAAT	ACAAAAAATA	AAAAAAAAT	TAGCTGGGTG	TGGTGGCAGG	4080
25	TGCCTGTAGT	CCCAGCTACT	TGGGAGGCTG	AGGCAGGAGA	ATCACTTGAA	CCCAGGAGGC	4140
	AGAGGTGCA	GTGAGCTGAG	ATCACGCCAC	TGCACTCCAG	CCTGGGTGAT	AGAGTAAGAC	4200
	TCTGTCTCAA	AGAAAAAAGA	AAAGAAAAGA	GACATGCAAA	TTAAAAACAG	CTACTCTCTT	4260
30	TCCCAGTGGC	TTCCATTAAT	TTCAGGAATT	TCCCCTTGAG	TGGCTTGGGT	TGAGAGGTTG	4320
	ATGACCTGTC	AGTTAGACTC	AAGAAAGCTG	AATCTAGGAG	AACCGCTATT	TTTTTTTTTAA	4380
35	GGGAATCTGC	CAAATTTTCT	TGCTGTGTAA	AGCTTCAATG	TGTATAGCTT	GGCTTTTGTA	4440
	GATTGTATTT	TCTTGAAACT	TAGCACACAG	GTATTTGCAG	AACTTCTAGG	AGTTAATTTT	4500
	TCTGCTCCAC	TCGGCTCTCA	GTCTTTTACG	GCATGGCCAA	GAGAGCTATT	TCTTGGCCTC	4560
40	CTGTGAAAAG	TTTCTTTCTT	CCTTTCTCCC	CACCTCCACA	TCCTTTCAGC	TCCTCTTTGT	4620
	ATCCAGGACA	AGAGGAAATG	GACTTCAGCC	ATGGTGAAAG	GAGTGTGAGT	TGGCTTTTGA	4680

	AGGAAAAGTT ATGGTAACGG AACAGTTCT AGAACAGAAA TCTTAGAAAT GACCAAATTT	4740
	TACTCAATGG CGCTTTAAGA GGCAGATATA ACTTATCCAA GGAATTAAAA CCCAAGCCAA	4800
5	CAGAAGAGAA TGTTCATAAA TTAATAATGAA AGCCACTGGG AAAATAGAGC CTGCCCATCA	4860
	TGAGAGGAAG AATAAGCAGA AATATGTGTA AAGCTTTAGA AGCCAAAATC AAAGTGAGAG	4920
10	ACATCTCGCC GAGAGAGGTG TGAGGAATGG AATAGGTGGC AGACATGTTG TGGAGCCTCC	4980
	TCACTGAAGA CTTTTAAACA TAGATATTCT TATTTATTTG AGTTGTCTTG GGAACCACCT	5040
	TATATTGCTT TTAAGTCATG TTGCTGATTC AAGAGTCTCG TAGGTCCTTC CAAGCATCCT	5100
15	TAGGGCCTCA GGTGAAAATA AAATCAGATA CAACCATGCA AAGCTCTAGG GAAGTGGGAA	5160
	GTTGAAAATG CCTAGGATCA GCTCTTTGGC TACCTGTGGT CACTCCTTTT ATTGTCGTCT	5220
20	GCCCAGGTGG CAGCTACAAG AAGATTGGCT ACTATGACAG CACCAAGGAT GATCTTTCCT	5280
	GGTCCAAAAC AGATAAATGG ATTGGTGAGT GGATCTTGTT TGTATTTTCC TTCAGCCCCCT	5340
	CTCGACAGTC AAGGGAAAAA GTCATGCCTT TGAGTGAGGA TGGAAATGGTA GAGACTGTTA	5400
25	GGTTGGAATG TGGCTGGCAG CTGGGCCAGG AGAAAGGGTT AAGTGAGAGT GAATACAACC	5460
	CCTAAGGCGT GGGTAGGGGA GACTGGTGTA TTTGGAGAGG GAATAGGCGG TGGTTAGTAC	5520
30	TATTTTTAAT GGTGCATTGC TGGGGTAACT GGGGATTAGA GGCAGGGGGT GGGCAGAGGG	5580
	CGGGAAATGG AAACCTCATT TGGGTTTCCC AGATGTCCTG GTGTCTTGAT ATATTTGAAC	5640
	CAGCTACTTC AAGCCCAGAG CTGTCTCTTT GTCTGTCTCT GTCAGGAAAA CGGTTGCTTA	5700
35	AACTATGGAG GAGGAGGGAA AACCTCATGT AATTGTCATC TGCCAAAATG TGCTTTTTAT	5760
	TTTTATATGT ATTTTTAAAA ATTTTCCTAT TTTTATGTAA TTTAGAGGTA GACGTGCAGT	5820
40	TGTGTTACAT GAATATATTG CATAGTGGTG AAGTCCGGGC GTTTAGTGTG CCTGTCACCC	5880
	GAACAGTGCA CCTTGTACCT AATAGGTAGT ATTACATCCC TCAAAATATA CTTTTTAAAG	5940

AGAGAAAGCA AGCAGTTATT CTTTGTGTAC TTGGTCTAAA TGATAGGACA TAGGAGAGAA 6000

ACTGAAGGTG GACAAAAGGA AGGACCTACT GATAAAAGAA AGCCTCCTTG AGAATGAAGG 6060

5 GGAGGCTCAA CCATTGAAGA TGGCTGCCGT CTGCCCTGCC CAGCAGATAT CCAGTCATTC 6120

CCAGCACTGC TGGAGTTTTG CCCTTTTTTT TTTTTTTTTT CAATTCGAAT TTAGGACAAT 6180

GTTCTGGATT GCTATAAATG CTGCATGGCC TAAATTATTC TTAAAAAAA AACTAAGCA 6240

10 AATTGAAATT AGTTTTTTTT GGTGAACTCT GACAAATTG AACTTCCCC TAATAATAAC 6300

TGGAAAACAT ATTTGGGAAT ATTACCCTGC CAGGATTAAA ATTCAGATT AGCTTTCCTT 6360

15 CTTTTTTTGT TTGTCTTAAG AATAGGTGTC CACACTAGAT ACTTCAAGGC CTTTTTAGCT 6420

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TTTTTAATGA TCCCCTTCTT TCTCCTCCCA TTTTCCTTTG CTGTAAGAAA GACAGAAAAA 6540

20 CTTAAGAAGC AAACAAAAAC AAAGACTACA ACTTTGGGGA CATGCCTCAG CATTTCCCAA 6600

CCTATGGATA GACCATTAC TCCATCTTCT CATCTCATTT CTGGTTGCTT CCTAACGGCC 6660

25 CCAGTGGCAC TGAGCATTCCT GCCTGCAGTA ACCTCTGTCC AGTGCAGTTA GGGCCTCATG 6720

TCCCCAGCCA ATGACTGAAT GTCCATCAGC AATCTAGTTC TTTGCCCTTT TCTCCTATCC 6780

CGTCTTCATT CCTTTGTCCT CCTTCCCTTC TCTTTTCCCT TCCCCTCTTC CTCCCCTGTG 6840

30 CCATGCAGGA GGGTCCCCC CAGCTGACCA GACCCTGGTC ATCAAGACAT TCCGCTTCCT 6900

GTCACAGAAA CTCTTTATCT CCGTCTCAGT TCTCTCCAGC CTGGGCATTG TCCTAGCTGT 6960

35 TGTCTGTCTG TCCTTTAACA TCTACAATC ACATGTCCGG TAAGTTTCTC TTCTGACGTT 7020

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40 CAGGGAAACC AGATATAACC CCCACTCCTA CTCCAAAGTA GCTAACGGGA GGAAAAAAGA 7200

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	AGCCTGTATT	CTAGTGGGGG	CCTGTGCTTG	GGAAGCCCTC	TGCAACTCCA	TCTTCAGCCC	7320
	CATGACTGCA	TTGCTCTGCC	TCTCAAGGCT	CCACTGTCTT	CTCCAATCCT	GTCTTCCTTT	7380
5	AGCCCCCTGGC	CCTGAAATTA	GGGTCATGCC	ATTGCGTGGT	ATTTGGAGAG	CTCAGCCTCC	7440
	CTGGAGAAGA	GGGGTAATTC	TCTCTCCCTC	TCACCCTCTC	CACCTCTGCC	CTAGTTATAT	7500
10	CCAGAACTCA	CAGCCCAACC	TGAACAACCT	GACTGCTGTG	GGCTGCTCAC	TGGCTTTAGC	7560
	TGCTGTCTTC	CCCCTGGGGC	TCGATGGTTA	CCACATTGGG	AGGAACCAGT	TTCTTTTCGT	7620
	CTGCCAGGTG	AGGAGGTGGT	GGGCAAATTC	CTTACAGGAT	GTGACTCTCC	CACCCGTCTC	7680
15	AGGAGCACCT	TCCATGATTT	ATGATTCTCT	GCCCTTCCTC	CTCAGCTTTC	CCTGACTCTT	7740
	GTCCCTGTTC	TTTCCTTCTA	GCATCACCCC	TCTGTTCTCT	GTTTGGCTCT	GTCCCTTCTT	7800
20	TCTGTGTCTG	CAGGCCATTT	TCATTCTGTA	GTTTACTTGT	CAGTTCCAAG	GTGCCATGG	7860
	CAGSCCTYGC	AGAGAAGAGG	AGGGAGCCAT	TGAAGGCAAA	GGAAGGGGAT	CTGCTCAAAG	7920
	GTCTCCTGAA	CAATGGTGGC	TTGTCTGTGG	TATGGGGGCT	GAGAATCAGA	ACTGTGGACT	7980
25	TTTTTTGGGA	GCCTTTGTTG	GGTTTGGAAG	GATAGAAGCA	GAGATGGAAA	CACAGCAGAG	8040
	AGTTGGGGGG	AAGGGACCAC	TGCCACACAG	GGGAGGAGGG	GCTCTGGGAC	TGTTGGTACA	8100
30	TGGAAGGTTT	TAGTGCTGTG	GGGAGAGGCC	AGCTTCAACA	GTGATAGTTG	AGTGGTTCTC	8160
	TTTTCCACTG	GTGGAAACAC	CCACTCTTTC	TCCTGATCTG	CCTGCCTGTC	CTTGCTCTCT	8220
	CTTTTTCCCTC	TGCTCTGTGC	TGTCCTGATC	ATACATCTGT	GCACATGGCA	TTTCCATGCA	8280
35	CATGCACATG	CAGTTCATCA	GGAATCCTCT	GTTCCCAGTG	AGGCCAGAGT	GCAGCTGGAG	8340
	AAGCAGACAA	TTAGCTGTAG	TGCAATAGGA	GAGGTTCCAG	AGTAGGGATC	TGCACAAAGT	8400
40	GCTTTGGGGG	CAAAGAAGGG	AACACAGTTC	ACTGCTGGCG	TGATTGGGTG	GACCTCACTG	8460
	AAGAGGTGGC	ATTTGAATAC	TGAAGGACAA	ATAGGATTTT	ATCAGCTAGA	GAAATAGAGG	8520

	AAGGCTACTT	CAGGGGCATA	GGGAGCATCG	TGTGGCTAGA	AAATACATGA	AAGAGAGTAG	8580
	ATGAAGAGAA	AGTGAGTAGT	TCAGCATGGC	TGGAGCGTGG	GGTAGGTGTG	GGGCTGGGAG	8640
5	ATGAGCCTAG	CTGGACAGGT	GGATGGGAGC	ATGTTGTGAA	GGGTCTGTGT	CATATCCAGA	8700
	AGTGTTTCAGG	CTATAACTTA	TAGATATTGG	GGAGTGGTTG	GAGGTTTTTTG	GCCACTAAAG	8760
	CCAGGAGGTT	TTAGCAAGAT	CACCCTGGTG	GTGTGGAAGT	AGAGGGTGGA	TGGGAGGAAT	8820
10	TGTTCAAGGT	GGGGAGACTG	CTCTCCTCCT	GCCGCTCCCC	GTCCTGCTCA	CATTTTCGCA	8880
	TCCTCCCTGT	GCCACCATGA	GCTCCCTGCC	CGTGCTCCCT	GCCCACTCTC	CCTTAGGGTT	8940
15	CTGCCCATCC	TTACTGCAGT	CCCGGCTACT	ACTCTACCCT	GTTCTGCCTG	TGCCCTCTCT	9000
	TCCTTTCTAG	GCCCGCCTCT	GGCTCCTGGG	CCTGGGCTTT	AGTCTGGGCT	ACGGTTCCAT	9060
	GTTACCAAG	ATTTGGTGGG	TCCACACGGT	CTTCACAAAG	AAGGAAGAAA	AGAAGGAGTG	9120
20	GAGGAAGGTG	AGCTGCTGCC	CAATCCTCAG	CCCCCARATC	CTTGGCTCCT	GGGGCACAGA	9180
	GCATTTTCCC	CTGACGTGCC	TGTTCTCCCC	ACATATTTAT	CCAGACTCTG	GAACCCTGGA	9240
25	AGCTGTATGC	CACAGTGGGC	CTGCTGGTGG	GCATGGATGT	CCTCACTCTC	GCCATCTGGC	9300
	AGATCGTGGA	CCCTCTGCAC	CGGACCATTG	AGGTACCACT	GGAGAGGAGG	TGCTATGGTC	9360
	AGGAGAATGA	GCAGGGCTCA	GTGGCCATCA	GGGCCCTGGG	GCTGTGTGTG	TCTTGAGGGA	9420
30	TGAAGCTACT	TGGAGAGAGT	GCCTTCCTCG	TATTGGAAGC	TCTTCCTTTC	CTTCCTAGAA	9480
	GGAGCCCCTC	ATAGGCCTCC	AGATTCAGCT	GAAGAAAGGA	AGGGGTGGGA	ATCTGGGAAG	9540
35	GGTGTGTAGA	ACTTCCAGGC	ATCAGGGAAA	GTGGGGAACA	AGCACCTCCA	AGGGTTCAGG	9600
	AAAACATTCT	TAGGCCTAGA	ATGAGATTTG	GCATCAGCAT	TGAGGGTCTC	ATAGGAAAAC	9660
	AGTTGGAAGC	CAGAGACTGA	GAAGCGTTGA	GGAGAGGAGG	GGAGGCTGGC	AACCATCTTT	9720
40	CTTGTGACCT	TGTTTCTGCC	CTAGACATTT	GCCAAGGAGG	AACCTAAGGA	AGATATTGAC	9780
	GTCTCTATTC	TGCCCCAGCT	GGAGCATTGC	AGCTCCAGGA	AGATGAATAC	ATGGCTTGGT	9840

	GTGTGGGATG	TGGGCAAAGG	AGGGCAGGGA	TGCACAAAGG	CAGGAGGGAA	GGCAGGGGTA	9900
	GAGGGCTTGG	AGGGAGAGGG	GTCTTTGGAA	GAGGAGGTAG	AGAGCTTGTC	AACCCAGTTT	9960
5	GAACACCCTA	CTCTTTGTTA	TTGCACTAAT	CTTTTCTGAG	AATAGGGGAG	AGTTGCTCTT	10020
	TTGCTATGAG	GAGCTTAGGG	CCCAAAGCAC	AGAAAGCACA	GATGAAGAAC	TTGTGTTTCAG	10080
10	CAGAGGAACA	AGTGGGGGTA	ACCCACCTC	CAGACTTGAC	ATTATCTTTT	AGATCCCCCT	10140
	TGGCCTTATT	AGCATTGTTC	GATTCATGGT	CACAAATTGC	AAACCTACCC	TCTGCCTGGA	10200
	AAGCCACCTT	CCCACCTGTA	GGGTAAGGGT	GAGGCATGTG	TGGCCCAGAC	TGGCCTATTT	10260
15	CTAGATATTC	AACAAGCCCT	TGCCTGACTG	ACAGCAGCTT	GCCACCATTG	CTTTCCTGTG	10320
	TGAATCCCAG	GAAAAAGTGA	TGTGGTCTGG	GCAAGTTGGG	TGGACATAAG	GGATAGGGGA	10380
20	CACAGGGTGA	GGTTTGCTAG	GTCAGAGGGG	TTGGATTGGA	GAGGAGGGCC	CCCTTTCCAT	10440
	TTCAGAGTAG	GTGAAGGGCA	GAGAGGGGAT	GGGGATTGAG	TGAGGAGCAT	TGTGGTCCTT	10500
	GTTGCTCAAG	TGACTCTCTC	CTGCCATCCT	AGGCATTTTC	TATGGTTAAC	AAGGGGCTGC	10560
25	TGCTGCTGCT	GGGAATCTTC	CTTGCTTATG	AGACCAAGAG	TGTGTCCACT	GAGAAGATCA	10620
	ATGATCACCG	GGCTGTGGGC	ATGGCTATCT	ACAATGTGGC	AGTGAGCACT	GACCCCATGG	10680
30	CATTGACCTT	GTAGGCTGAC	CACAGCAGCC	CAGATATAGA	GGACTAGGAA	GAATCAATGC	10740
	TAGATCTGGG	ATCGGTTGCT	TAGAAGTCTT	AAAAAGTTTG	TTAATTCTTC	AGGTCTATAA	10800
	AGCACTTTAC	AGTTTACAAA	GCTCACTACA	GACATTGTAT	CATTAATCTT	GCAACTACCC	10860
35	AGTGAAGTAG	ATATTAGTAT	CCCCACTTTA	TAGGTGAGGA	AACAGAAACA	CAGAGACGTT	10920
	AAATTGCTTG	TCTGTGGTTA	ATGGGCTGGA	CTCTATTGAC	ATTCCTGCC	AGGGACCGAC	10980
40	TCTGGAGGAC	CCGGAATCTG	TGCATAGAGA	TCCTGGGAGT	TCCTGCCTTG	AGGGGAGGGG	11040
	TTAACCAAGA	GTGAAACTG	GTTTGGGACA	GTTTGAGATT	TTTCTCAATC	TATATTGAGG	11100

ATGATCCTGA ATTTGGATCC TTTTCAAAGG GAAAGTTCAC CAGGAAACTG TCTGCATAGA 11160
 CTCCCTCCCA TGGGAAGTAA ACTCTGGATC TTGTCTGAGC CTGCAGACCT GAGACTCCCT 11220
 5 CAATGTGTCT TTCCCTCTAG GTCCTGTGCC TCATCACTGC TCCTGTCACC ATGATTCTGT 11280
 CCAGCCAGCA GGATGCAGCC TTTGCCTTTG CCTCTCTTGC CATAGTTTTT TCCTCCTATA 11340
 TCACTCTTGT TGTGCTCTTT GTGCCCCAAG TAAGGATCTG GCTTTTCTCC CACCCTCTTT 11400
 10 GTTCCCATGT TCCCTCCATC CCTCCTTCCT ATATTACTGA GTTCCTCTGC CCTTCCGTTC 11460
 ACCCTCCTCT CACTCCTCCC CTTGTTTTGG GCCCAACTCT TATCAGCATT CCTTCCACCT 11520
 15 CCAACCTTCC ATCAGCCAGT CACTAGTACA GTCCTTGCTG GGCCACCCCA CGCCCAAACA 11580
 TTTGCCCCCA GATGCGCAGG CTGATCACCC GAGGGGAATG GCAGTCGGAG GCGCAGGACA 11640
 CCATGAAGAC AGGGTCATCG ACCAACAACA ACGAGGAGGA GAAGTCCCGG CTGTTGGAGA 11700
 20 AGGAGAACCG TGAAGTGGAA AAGATCATTG CTGAGGTGCG GGGGTGGGTG TCAGGGTAGG 11760
 GTGTTGGAGT GGTCCAGGAG GCTTGCGTCT TAGCTTGGGT TGTCTGAAGC CAAGCCTGAG 11820
 25 ATACAGGGTC AGATGTTCTT GGCTCATGGA GGGAGGGTCC TAGGAGACAA CCTGTAAGGA 11880
 GTGAATGGAG CAGCATAGGG GAGGGGAAAG GGCTGAGCAA GATTCTATCT CAGGCAAAT 11940
 CCAGTGTTGG CCTGGCAGGT GGAAGGGCTC TGGAGTGGGA GCTATGTGGT TGACTCAGCC 12000
 30 TCCTTAAGGC AAGAGGATGG CTGTTGGCTG TAGGTGACAA CTGGAGAGAG GCAGCTGTGA 12060
 GCCTCTAGTA GTCAACACTC ACAGCAGCTG GGTGTAGCAT GCAGCCCCAG CATAAAGGAC 12120
 35 CTGGGCAGGC GTTCACTGTG CCCCAGGCTG TCATTAGGGG CTGGTGCAAT GCCAAAGAGA 12180
 GGGATGTTCC AACTGGGTTG ACACATCTCT CTGATTTATT GGAAGCTCTG TGCACTGACT 12240
 TTTCTCTCCT TCCCCACTTT TTCCTTTTGT TTTTAAATTC TCTCTTATTT CCCTGATCGC 12300
 40 ATTTTTTCTA TCGGTATCCT TATGTTCTCT GGCTTTTCTT GTTCTGTTTT GATTTCTCCT 12360
 TTTAATTTAT TCTGTCCACT TACCCTACGT CCTCCCCCTA CATTTTTCTG TGCCCTTCCT 12420

	CTCTTTCCCT	GTGCCCTTCC	TCTCTTTCCC	TCCTCCCCAC	TCCTTCATCA	CCTCCTCTTC	12480
	TCCTACTATC	CCAATTGTGC	TTCTTCCTCC	AGAAAGAGGA	GCGTGTCTCT	GAAGTGCGCC	12540
5	ATCAACTCCA	GTCTCGGCAG	CAGCTCCGCT	CCCGGCGCCA	CCCACCGACA	CCCCCAGAAC	12600
	CCTCTGGGGG	CCTGCCCAGG	GGACCCCCTG	AGCCCCCCGA	CCGGCTTAGC	TGTGATGGGA	12660
10	GTCGAGTGCA	TTTGCTTTAT	AAGTGAGGGT	AGGGTGAGGG	AGGACAGGCC	AGTAGGGGGA	12720
	GGGAAAGGGA	GAGGGGAAGG	GCAGGGGACT	CAGGAAGCAG	GGGGTCCCCA	TCCCCAGCTG	12780
	GGAAGAACAT	GCTATCCAAT	CTCATCTCTT	GTAAATACAT	GTCCCCCTGT	GAGTTCTGGG	12840
15	CTGATTTGGG	TCTCTCATAC	CTCTGGGAAA	CAGACCTTTT	TCTCTCTTAC	TGCTTCATGT	12900
	AATTTTGTAT	CACCTCTTCA	CAATTTAGTT	CGTACCTGGC	TTGAAGCTGC	TCAGTGTCTCA	12960
20	CACGCTGCCT	CCTCAGCAGC	CTCACTGCAT	CTTTCTCTTC	CCATGCAACA	CCCTCTTCTA	13020
	GTTACCACGG	CAACCCCTGC	AGCTCCTCTG	CCTTTGTGCT	CTGTTCTCTGT	CCAGCAGGGG	13080
	TCTCCCAACA	AGTGCTCTTT	CCACCCCAAA	GGGGCCTCTC	CTTTTCTCCA	CTGTCATAAT	13140
25	CTCTTTCCAT	CTTACTTGCC	CTTCTATACT	TTCTCACATG	TGGCTCCCCC	TGAATTTTGC	13200
	TTCTTTGGG	AGCTCATTCT	TTTCGCCAAG	GCTCACATGC	TCCTTGCCCTC	TGCTCTGTGC	13260
30	ACTCACGCTC	AGCACACATG	CATCCTCCCC	TCTCCTGCGT	GTGCCCCACTG	AACATGCTCA	13320
	TGTGTACACA	CGCTTTTCCC	GTATGCTTTC	TTCATGTTCA	GTCACATGTG	CTCTCGGGTG	13380
	CCCTGCATTC	ACAGCTACGT	GTGCCCCCTCT	CATGGTCATG	GGTCTGCCCT	TGAGCGTGTT	13440
35	TGGGTAGGCA	TGTGCAATTT	GTCTAGCATG	CTGAGTCATG	TCTTTCCTAT	TTGCACACGT	13500
	CCATGTTTAT	CCATGTACTT	TCCCTGTGTA	CCCTCCATGT	ACCTTG TGTA	CTTCTTCCCC	13560
40	TTAAATCATG	GTATTCTTCT	GACAGAGCCA	TATGTACCCT	ACCCTGCACA	TTGTTATGCA	13620
	CTTTTCCCCA	ATTCATGTTT	GGTGGGGCCA	TCCACACCCT	CTCCTTGTC	AGAATCTCC	13680

	ATTTCTGCTC	AGATTCCCC	CATCTCCATT	GCATTCATGT	ACTACCCTCA	GTCTACACTC	13740
	ACAATCATCT	TCTCCCAAGA	CTGCTCCCTT	TTGTTTTGTG	TTTTTTTGAG	GGGAATTAAG	13800
5	GAAAAATAAG	TGGGGGCAGG	TTTGGAGAGC	TGCTTCCAGT	GGATAGTTGA	TGAGAATCCT	13860
	GACCAAAGGA	AGGCACCCTT	GACTGTTGGG	ATAGACAGAT	GGACCTATGG	GGTGGGAGGT	13920
	GGTGTCCTT	TCACACTGTG	GTGTCTCTTG	GGGAAGGATC	TCCCCGAATC	TCAATAAACC	13980
10	AGTGAACAGT	GTGACTCGGC	ACCTTGCAGT	CTTCCTGTGA	ACAGAATGGG	CTTCAATCCA	14040
	AGAAGGGAGG	CTCAGAGGAC	TCCAAGTTCA	TGAAAAGGCA	TTAAAGCGGA	GGGTGAAAAG	14100
15	AGGTGTTTTA	TTGATCCATT	GAGGGCTTAG	CAGAATGAAG	CAGGACATGA	TTAAGTCTGA	14160
	GATTAGTGAG	TGAGGACACT	ACTGGTTAAA	AGTGTGGGCT	CTGGAGTCAG	ACTGCCAGGG	14220
	TATCAGATCC	AACCACATGC	AAACATTTTC	TTAGTCTCTA	TTCCCCATGT	CCTCATTTAT	14280
20	GAAAATGAGA	ATAACAGTAA	TACATTCCTC	CATAGGTTGG	GTACAAAGAC	TATTATAAAT	14340
	TGTGCATTCA	GGTGCCTAGG	TTGGCCCTTG	GGCCATGGTA	TATGTTGCGT	GAATGTTAGC	14400
25	CTCTGTCCCT	GCTGTTTAAT	GAGTTCCTTG	ACAGTAGTGG	GCATGTATTG	GGAGCCTGGA	14460
	GCAAGTGCCT	AAGCATCCCC	TCTAGGGACG	CTCCTTCCCA	GGAACTAAGA	AGAGTAAAAG	14520
	AATGATGACT	GCTAGAAGGT	AATGGATGAG	ATGGCTGCTG	AGTGCTTCCA	ACCTTAAACA	14580
30	TCTTTGTTTA	GGAACCTCTGA	GCATCTTGGA	AATAATTTGC	TATCAAACCTG	AAAAAAAATC	14640
	TTGAATGGAC	AAGGGCAAAA	ACATTTGCCT	GAGACTTTAA	ACATTTTTTTG	TGTCATCTTG	14700
35	GAGAGTGCTT	TTTTGAAGCT	CAAATTTTCT	TTTATTTTGG	CACTGATTTT	TAAAGTGATT	14760
	CTCAGATTTT	TGTAAGACAG	CTGCAAGGGT	TGGATGGGCC	CTGTCATTCA	CTGACCTGTT	14820
	AAGAGCCAAT	TTCTGAACTT	CCACTAAAGC	ATGGGCTGGT	TGAATCTTAG	ACCAGTACTT	14880
40	GAAAAACTTT	CCACTGTGAT	TATCCACCTT	GGACCAGTTG	GACTTAATTT	GAGTCTCTCT	14940
	TCTTCCCACA	GTGAAATATC	CGCTAGGAAA	AGAGAAGAAG	TCTATGGAGT	AGATAAGCCT	15000

	GCAGTTTGA	AAATGAATAG	TTGGCATCAG	AACAGCAGCA	GGAGGCTGGG	TGTGGTGGCT	15060
	CACGCCTGTA	ATCCCAGCAC	TTTGGGAGGC	TGAGGTGGGT	GGATCACGAG	GTCAGGAGTT	15120
5	CAAGACCAGC	CTGGCCAAGA	TGGCGAAACC	CTGTCTCTAC	TAAAAATACA	AAAATTAGCT	15180
	GGGCGTGATG	GTGGGTGCCT	GTAATCTCAG	CTACTCGGGA	GGCTGAGGCA	GATAATTGCT	15240
10	TGAACCCAGG	AGATGAAGGT	TGCAGTGAGT	TTGTGCCACT	GCACTCCAGC	CTGGGCGACA	15300
	GAGTGAGACT	GTCTCAAAAA	AAAAAAAAAA	GAAAAAAAAA	AAAGAAACAA	CAGTAGCAGG	15360
	AGCTATAGAA	CAGCCCTGGG	TAGAACCCTAA	AAGACCCAAA	TTATCATCTC	AAACTTGCAT	15420
15	TGCACTTAAG	TGGGCTGTAA	ATTATAAACA	AAGGGTGAAA	AGTTCTACTG	TGGCCAAAGG	15480
	TAAGCCAGAC	ACTCTGCTAG	CAGGAGTGCA	GGAGTCGAGA	GCCAAACGGT	GCGGCTAGCA	15540
20	GAGTGCCCAG	TGCAAAGGGG	TGGGAAGGAG	TGAGATTGAG	AATATTAAAA	AGGTACTTAG	15600
	AAGAGAACTT	GTAAGATTTT	TACTGGCCAA	ATTTAAAACA	TGACTGAGCA	CTATTTTTTCA	15660
	TACAGGCCTC	CTACTAATAA	GAAAACAATT	TTGAGATAAC	TACTTATTTG	AGTTCACAGT	15720
25	TAATGTTCCCT	GATGATTAAG	ATCAGTTGCA	AATGTTTCATC	TGTCAATGCT	TATCTACAAT	15780
	GAGACTTCAT	GTATTCATTT	CTGAAAGTGT	CTTTTCAGGG	TGAATGGTGC	TATTGATTAG	15840
30	CACTAATACT	AATTATTAGT	ACATTATATA	TAATTACAAT	GAGATATACA	CACACATACA	15900
	CACACACATA	TATACATATA	CACACACACA	ATGATATATA	ATTAATATAT	AATTGTACCC	15960
	CAAGGGGTGC	AAAGGAGATG	TGTTGCCAGG	TGGAGAGGCT	ACCGCTTGGC	AGTTCTGGGA	16020
35	GGACTTGCTC	CCTGTGCACT	GTGAGGCAGG	CTTTGCCTTT	CAGACCTGCC	TTTGGGTAGG	16080
	GTTTCAGATCA	CTTTCTAACT	CTGGAATGTC	CTAGAATGTA	GACTGCCTGC	AGGCTTCCAT	16140
40	GTCCCCTGCT	TTTCCCTGAC	TTAGCCTGTT	GCCTCCCTGC	CCTCCTGTTG	GTTGTCTACC	16200
	AGTAGAGAGC	ACTTTGTGTG	CACTTGGCTG	CTACATTAGT	TAGGTGATCT	TCAACAAGTG	16260

TTGATGGTGA GTTGCTGTGG CAGGTGCTTT TTTTGGCACT GAGGCAAAAT GGTGAGTAAG 16320
ATGGCTTTCA AGCGTTGTAC CTTCTCGACG TGGGAAGATG ACCAGTAAGC AGAAAAACAA 16380
5 ACGAGATCAC TTAAGAGAGC AACCAGGAGT GTTGGGCATC TCACAGCCAT TAGCTCTGGT 16440
GTGAAGGACA AATCTAAAAG CAAGGGGACT GTGTGTTTCAT TTTCTGGGGT CACAAAACATA 16500
AGGAGCAAAG CCAGTATTCA AACTGCATAT ATTATTATCT ATTGCCACAA AACCTGTTAC 16560
10 CCTAAATGGC TTCAGACAAC AATAATCATT TATTATCCAT CATGGTTTTT GTGGGCTAGA 16620
AATTCAGATA GGGTACAGTG GGGAGGGTTC ACCCTGCTCC ACAGCATCTG GAAGATCTGA 16680
15 AGTCTGAGGG TTGTTGTCCA AAAGATC 16707

20 (2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

ATGCGCGCCG GCAGCCAACA TGCTGCTGCT GCTGCTGGTG CCTCTCTTCC

50

(2) INFORMATION FOR SEQ ID NO: 63:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GGTCATCCAG CGTTGAGGTG AAGAC

25

5

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GAAGGTTGCC AGATTATACA TCCGC

25

20

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

CCACGATGAT TCGAGCATCT TGACG

25

35

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

5

CTGGTTCCTC CCAATGTG

18

(2) INFORMATION FOR SEQ ID NO: 67:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

20

CCAGTGGACT ATGAGATTGA G

21

(2) INFORMATION FOR SEQ ID NO: 68:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

35

CTGGTTCCTC CCAATGTG

18

(2) INFORMATION FOR SEQ ID NO: 69:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CCAGTGGACT ATGAGATTGA G

21

10

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 2700 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

30

(A) NAME/KEY: CDS
(B) LOCATION:1..2700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC 48
35 Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
1 5 10 15

GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC 96
Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
40 20 25 30

ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG 144
Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg

	35		40		45																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				</
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	Ser	Pro	Ala	Leu	Ser	Asn	Arg	Gln	Arg	Phe	Pro	Thr	Phe	Phe	Arg	Thr	
	210					215					220						
	CAC	CCA	TCA	GCC	ACA	CTC	CAC	AAC	CCT	ACC	CGC	GTG	AAA	CTC	TTT	GAA	720
5	His	Pro	Ser	Ala	Thr	Leu	His	Asn	Pro	Thr	Arg	Val	Lys	Leu	Phe	Glu	
	225					230				235					240		
	AAG	TGG	GGC	TGG	AAG	AAG	ATT	GCT	ACC	ATC	CAG	CAG	ACC	ACT	GAG	GTC	768
10	Lys	Trp	Gly	Trp	Lys	Lys	Ile	Ala	Thr	Ile	Gln	Gln	Thr	Thr	Glu	Val	
					245					250					255		
	TTC	ACT	TCG	ACT	CTG	GAC	GAC	CTG	GAG	GAA	CGA	GTG	AAG	GAG	GCT	GGA	816
	Phe	Thr	Ser	Thr	Leu	Asp	Asp	Leu	Glu	Glu	Arg	Val	Lys	Glu	Ala	Gly	
					260				265					270			
15	ATT	GAG	ATT	ACT	TTC	CGC	CAG	AGT	TTC	TTC	TCA	GAT	CCA	GCT	GTG	CCC	864
	Ile	Glu	Ile	Thr	Phe	Arg	Gln	Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	
		275					280						285				
20	GTC	AAA	AAC	CTG	AAG	CGC	CAG	GAT	GCC	CGA	ATC	ATC	GTG	GGA	CTT	TTC	912
	Val	Lys	Asn	Leu	Lys	Arg	Gln	Asp	Ala	Arg	Ile	Ile	Val	Gly	Leu	Phe	
		290					295				300						
	TAT	GAG	ACT	GAA	GCC	CGG	AAA	GTT	TTT	TGT	GAG	GTG	TAC	AAG	GAG	CGT	960
25	Tyr	Glu	Thr	Glu	Ala	Arg	Lys	Val	Phe	Cys	Glu	Val	Tyr	Lys	Glu	Arg	
	305					310				315					320		
	CTC	TTT	GGG	AAG	AAG	TAC	GTC	TGG	TTC	CTC	ATT	GGG	TGG	TAT	GCT	GAC	1008
30	Leu	Phe	Gly	Lys	Lys	Tyr	Val	Trp	Phe	Leu	Ile	Gly	Trp	Tyr	Ala	Asp	
					325					330					335		
	AAT	TGG	TTC	AAG	ATC	TAC	GAC	CCT	TCT	ATC	AAC	TGC	ACA	GTG	GAT	GAG	1056
	Asn	Trp	Phe	Lys	Ile	Tyr	Asp	Pro	Ser	Ile	Asn	Cys	Thr	Val	Asp	Glu	
				340					345					350			
35	ATG	ACT	GAG	GCG	GTG	GAG	GGC	CAC	ATC	ACA	ACT	GAG	ATT	GTC	ATG	CTG	1104
	Met	Thr	Glu	Ala	Val	Glu	Gly	His	Ile	Thr	Thr	Glu	Ile	Val	Met	Leu	
				355				360					365				
40	AAT	CCT	GCC	AAT	ACC	CGC	AGC	ATT	TCC	AAC	ATG	ACA	TCC	CAG	GAA	TTT	1152
	Asn	Pro	Ala	Asn	Thr	Arg	Ser	Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	Phe	
		370					375				380						

	GTG GAG AAA CTA ACC AAG CGA CTG AAA AGA CAC CCT GAG GAG ACA GGA	1200
	Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly	
	385 390 395 400	
5	GGC TTC CAG GAG GCA CCG CTG GCC TAT GAT GCC ATC TGG GCC TTG GCA	1248
	Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala	
	405 410 415	
	CTG GCC CTG AAC AAG ACA TCT GGA GGA GGC GGC CGT TCT GGT GTG CGC	1296
10	Leu Ala Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg	
	420 425 430	
	CTG GAG GAC TTC AAC TAC AAC AAC CAG ACC ATT ACC GAC CAA ATC TAC	1344
	Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr	
15	435 440 445	
	CGG GCA ATG AAC TCT TCG TCC TTT GAG GGT GTC TCT GGC CAT GTG GTG	1392
	Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val	
	450 455 460	
20	TTT GAT GCC AGC GGC TCT CGG ATG GCA TGG ACG CTT ATC GAG CAG CTT	1440
	Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu	
	465 470 475 480	
25	CAG GGT GGC AGC TAC AAG AAG ATT GGC TAC TAT GAC AGC ACC AAG GAT	1488
	Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp	
	485 490 495	
	GAT CTT TCC TGG TCC AAA ACA GAT AAA TGG ATT GGA GGG TCC CCC CCA	1536
30	Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro	
	500 505 510	
	GCT GAC CAG ACC CTG GTC ATC AAG ACA TTC CGC TTC CTG TCA CAG AAA	1584
	Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys	
35	515 520 525	
	CTC TTT ATC TCC GTC TCA GTT CTC TCC AGC CTG GGC ATT GTC CTA GCT	1632
	Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala	
	530 535 540	
40	GTT GTC TGT CTG TCC TTT AAC ATC TAC AAC TCA CAT GTC CGT TAT ATC	1680
	Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile	
	545 550 555 560	

	CAG AAC TCA CAG CCC AAC CTG AAC AAC CTG ACT GCT GTG GGC TGC TCA	1728
	Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser	
	565 570 575	
5	CTG GCT TTA GCT GCT GTC TTC CCC CTG GGG CTC GAT GGT TAC CAC ATT	1776
	Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile	
	580 585 590	
10	GGG AGG AAC CAG TTT CCT TTC GTC TGC CAG GCC CGC CTC TGG CTC CTG	1824
	Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu	
	595 600 605	
	GGC CTG GGC TTT AGT CTG GGC TAC GGT TCC ATG TTC ACC AAG ATT TGG	1872
15	Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp	
	610 615 620	
	TGG GTC CAC ACG GTC TTC ACA AAG AAG GAA GAA AAG AAG GAG TGG AGG	1920
	Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg	
20	625 630 635 640	
	AAG ACT CTG GAA CCC TGG AAG CTG TAT GCC ACA GTG GGC CTG CTG GTG	1968
	Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val	
	645 650 655	
25	GGC ATG GAT GTC CTC ACT CTC GCC ATC TGG CAG ATC GTG GAC CCT CTG	2016
	Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu	
	660 665 670	
30	CAC CGG ACC ATT GAG ACA TTT GCC AAG GAG GAA CCT AAG GAA GAT ATT	2064
	His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile	
	675 680 685	
	GAC GTC TCT ATT CTG CCC CAG CTG GAG CAT TGC AGC TCC AGG AAG ATG	2112
35	Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met	
	690 695 700	
	AAT ACA TGG CTT GGC ATT TTC TAT GGT TAC AAG GGG CTG CTG CTG CTG	2160
	Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu	
40	705 710 715 720	
	CTG GGA ATC TTC CTT GCT TAT GAG ACC AAG AGT GTG TCC ACT GAG AAG	2208
	Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys	

		725		730		735		
	ATC AAT GAT CAC CGG GCT GTG GGC ATG GCT ATC TAC AAT GTG GCA GTC							2256
	Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val							
5		740		745		750		
	CTG TGC CTC ATC ACT GCT CCT GTC ACC ATG ATT CTG TCC AGC CAG CAG							2304
	Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln							
		755		760		765		
10	GAT GCA GCC TTT GCC TTT GCC TCT CTT GCC ATA GTT TTC TCC TCC TAT							2352
	Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr							
		770		775		780		
15	ATC ACT CTT GTT GTG CTC TTT GTG CCC AAG ATG CGC AGG CTG ATC ACC							2400
	Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr							
		785		790		795		800
	CGA GGG GAA TGG CAG TCG GAG GCG CAG GAC ACC ATG AAG ACA GGG TCA							2448
20	Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser							
		805		810		815		
	TCG ACC AAC AAC AAC GAG GAG GAG AAG TCC CGG CTG TTG GAG AAG GAG							2496
	Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu							
25		820		825		830		
	AAC CGT GAA CTG GAA AAG ATC ATT GCT GAG AAA GAG GAG CGT GTC TCT							2544
	Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser							
		835		840		845		
30	GAA CTG CGC CAT CAA CTC CAG TCT CGG CAG CAG CTC CGC TCC CGG CGC							2592
	Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg							
		850		855		860		
35	CAC CCA CCG ACA CCC CCA GAA CCC TCT GGG GGC CTG CCC AGG GGA CCC							2640
	His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro							
		865		870		875		880
	CCT GAG CCC CCC GAC CGG CTT AGC TGT GAT GGG AGT CGA GTG CAT TTG							2688
40	Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu							
		885		890		895		
	CTT TAT AAG TGA							2700

Leu Tyr Lys *

5 (2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 899 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

15

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 1 5 10 15

20

Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 20 25 30

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 35 40 45

25

Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
 50 55 60

Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
 65 70 75 80

30

Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
 85 90 95

35

Val Asn Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala
 100 105 110

Leu Phe Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro
 115 120 125

40

Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu
 130 135 140

Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro

145	150	155	160
Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile	165	170	175
5	Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala	180	185 190
10	Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser	195	200 205
	Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr	210	215 220
15	His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu	225	230 235 240
	Lys Trp Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val	245	250 255
20	Phe Thr Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly	260	265 270
	Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro	275	280 285
25	Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe	290	295 300
30	Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg	305	310 315 320
	Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp	325	330 335
35	Asn Trp Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu	340	345 350
	Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu	355	360 365
40	Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe	370	375 380

	Val	Glu	Lys	Leu	Thr	Lys	Arg	Leu	Lys	Arg	His	Pro	Glu	Glu	Thr	Gly	385	390	395	400
5	Gly	Phe	Gln	Glu	Ala	Pro	Leu	Ala	Tyr	Asp	Ala	Ile	Trp	Ala	Leu	Ala	405	410	415	
	Leu	Ala	Leu	Asn	Lys	Thr	Ser	Gly	Gly	Gly	Gly	Arg	Ser	Gly	Val	Arg	420	425	430	
10	Leu	Glu	Asp	Phe	Asn	Tyr	Asn	Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	435	440	445	
	Arg	Ala	Met	Asn	Ser	Ser	Ser	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	450	455	460	
15	Phe	Asp	Ala	Ser	Gly	Ser	Arg	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	465	470	475	480
	Gln	Gly	Gly	Ser	Tyr	Lys	Lys	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	485	490	495	
	Asp	Leu	Ser	Trp	Ser	Lys	Thr	Asp	Lys	Trp	Ile	Gly	Gly	Ser	Pro	Pro	500	505	510	
25	Ala	Asp	Gln	Thr	Leu	Val	Ile	Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys	515	520	525	
	Leu	Phe	Ile	Ser	Val	Ser	Val	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	530	535	540	
30	Val	Val	Cys	Leu	Ser	Phe	Asn	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	545	550	555	560
	Gln	Asn	Ser	Gln	Pro	Asn	Leu	Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	565	570	575	
	Leu	Ala	Leu	Ala	Ala	Val	Phe	Pro	Leu	Gly	Leu	Asp	Gly	Tyr	His	Ile	580	585	590	
40	Gly	Arg	Asn	Gln	Phe	Pro	Phe	Val	Cys	Gln	Ala	Arg	Leu	Trp	Leu	Leu	595	600	605	

Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp
 610 615 620

Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg
 5 625 630 635 640

Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val
 645 650 655

10 Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu
 660 665 670

His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile
 675 680 685

15 Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met
 690 695 700

Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu
 20 705 710 715 720

Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys
 725 730 735

25 Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val
 740 745 750

Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln
 755 760 765

30 Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr
 770 775 780

Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr
 35 785 790 795 800

Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser
 805 810 815

40 Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu
 820 825 830

Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser

835

840

845

Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg
850 855 860

5

His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly
865 870 875

10

Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His
885 890 895

Leu Tyr Lys

15

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 2518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

30

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..294

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

40

ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CC
Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pr
1 5 10 15

GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CA
Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gl

	20	25	30	
	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG			144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg			
5	35	40	45	
	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG			192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu			
	50	55	60	
10	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG			240
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys			
	65	70	75	80
15	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT			288
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys			
	85	90	95	
	GTG TGA TCCAGGCCAA GCCACCAAGT ACCTATATGA GCTGCTCTAC AACGACCCTA			344
20	Val *			
	TCAAGATCAT CCTTATGCCT GGCTGCAGCT CTGTCTCCAC GCTGGTGGCT GAGGCTGCTA			404
25	GGATGTGGAA CCTCATTGTG CTTTCCTATG GCTCCAGCTC ACCAGCCCTG TCAAACCGGC			464
	AGCGTTTCCC CACTTCTTTC CGAACGCACC CATCAGCCAC ACTCCACAAC CCTACCCGCG			524
	TGAAACTCTT TGAAAAGTGG GGCTGGAAGA AGATTGCTAC CATCCAGCAG ACCACTGAGG			584
30	TCTTCACTTC GACTCTGGAC GACCTGGAGG AACGAGTGAA GGAGGCTGGA ATTGAGATTA			644
	CTTTCCGCCA GAGTTTCTTC TCAGATCCAG CTGTGCCCCGT CAAAAACCTG AAGCGCCAGG			704
35	ATGCCCGAAT CATCGTGGA CTTTTCTATG AGACTGAAGC CCGGAAAGTT TTTTGTGAGG			764
	TGTACAAGGA GCGTCTCTTT GGGAAGAAGT ACGTCTGGTT CCTCATTGGG TGGTATGCTG			824
	ACAATTGGTT CAAGATCTAC GACCCTTCTA TCAACTGCAC AGTGGATGAG ATGACTGAGG			884
40	CGGTGGAGGG CCACATCACA ACTGAGATTG TCATGCTGAA TCCTGCCAAT ACCCGCAGCA			944
	TTTCCAACAT GACATCCCAG GAATTTGTGG AGAAACTAAC CAAGCGACTG AAAAGACACC			1004

	CTGAGGAGAC	AGGAGGCTTC	CAGGAGGCAC	CGCTGGCCTA	TGATGCCATC	TGGGCCTTGG	1064
	CACTGGCCCT	GAACAAGACA	TCTGGAGGAG	GCGGCCGTTC	TGGTGTGCGC	CTGGAGGACT	1124
5	TCAACTACAA	CAACCAGACC	ATTACCGACC	AAATCTACCG	GGCAATGAAC	TCTTCGTCCT	1184
	TTGAGGGTGT	CTCTGGCCAT	GTGGTGTTTG	ATGCCAGCGG	CTCTCGGATG	GCATGGACGC	1244
10	TTATCGAGCA	GCTTCAGGGT	GGCAGCTACA	AGAAGATTGG	CTACTATGAC	AGCACCAAGG	1304
	ATGATCTTTC	CTGGTCCAAA	ACAGATAAAT	GGATTGGAGG	GTCCCCCCCCA	GCTGACCAGA	1364
	CCCTGGTCAT	CAAGACATTC	CGCTTCCTGT	CACAGAAACT	CTTTATCTCC	GTCTCAGTTC	1424
15	TCTCCAGCCT	GGGCATTGTC	CTAGCTGTTG	TCTGTCTGTC	CTTTAACATC	TACAACTCAC	1484
	ATGTCCGTTA	TATCCAGAAC	TCACAGCCCA	ACCTGAACAA	CCTGACTGCT	GTGGGCTGCT	1544
20	CACTGGCTTT	AGCTGCTGTC	TTCCCCCTGG	GGCTCGATGG	TTACCACATT	GGGAGGAACC	1604
	AGTTTCCTTT	CGTCTGCCAG	GCCCGCCTCT	GGCTCCTGGG	CCTGGGCTTT	AGTCTGGGCT	1664
	ACGGTTCCAT	GTTACCAAG	ATTTGGTGGG	TCCACACGGT	CTTCACAAAG	AAGGAAGAAA	1724
25	AGAAGGAGTG	GAGGAAGACT	CTGGAACCCT	GGAAGCTGTA	TGCCACAGTG	GGCCTGCTGG	1784
	TGGGCATGGA	TGTCCTCACT	CTCGCCATCT	GGCAGATCGT	GGACCCCTCTG	CACCGGACCA	1844
30	TTGAGACATT	TGCCAAGGAG	GAACCTAAGG	AAGATATTGA	CGTCTCTATT	CTGCCCCAGC	1904
	TGGAGCATTG	CAGCTCCAGG	AAGATGAATA	CATGGCTTGG	CATTTTCTAT	GGTTACAAGG	1964
	GGCTGCTGCT	GCTGCTGGGA	ATCTTCCTTG	CTTATGAGAC	CAAGAGTGTG	TCCACTGAGA	2024
35	AGATCAATGA	TCACCGGGCT	GTGGGCATGG	CTATCTACAA	TGTGGCAGTC	CTGTGCCTCA	2084
	TCACTGCTCC	TGTCACCATG	ATTCTGTCCA	GCCAGCAGGA	TGCAGCCTTT	GCCTTTGCCT	2144
40	CTCTTGCCAT	AGTTTTCTCC	TCCTATATCA	CTCTTGTTGT	GCTCTTTGTG	CCCAAGATGC	2204
	GCAGGCTGAT	CACCCGAGGG	GAATGGCAGT	CGGAGGCGCA	GGACACCATG	AAGACAGGGT	2264

CATCGACCAA CAACAACGAG GAGGAGAAGT CCCGGCTGTT GGAGAAGGAG AACCGTGAAC 2324
 TGGAAAAGAT CATTGCTGAG AAAGAGGAGC GTGTCTCTGA ACTGCGCCAT CAACTCCAGT 2384
 5 CTCGGCAGCA GCTCCGCTCC CGGCGCCACC CACCGACACC CCCAGAACCC TCTGGGGGCC 2444
 TGCCCAGGGG ACCCCCTGAG CCCCCCGACC GGCTTAGCTG TGATGGGAGT CGAGTGCATT 2504
 TGCTTTATAA GTGA 2518

10

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

25

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 1 5 10 15

Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 20 25 30

30

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 35 40 45

Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
 50 55 60

35

Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
 65 70 75 80

Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
 85 90 95

40

Val

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2679 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

20

(A) NAME/KEY: CDS

(B) LOCATION:1..2679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

25	ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
	Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
	1 5 10 15	
	GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
30	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
	20 25 30	
	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
35	35 40 45	
	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
	50 55 60	
40	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
	65 70 75 80	

	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	
	85 90 95	
5	GAA CGG CGC GCA GTG TAC ATC GGG GCA CTG TTT CCC ATG AGC GGG GGC	336
	Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly	
	100 105 110	
10	TGG CCA GGG GGC CAG GCC TGC CAG CCC GCG GTG GAG ATG GCG CTG GAG	384
	Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu	
	115 120 125	
	GAC GTG AAT AGC CGC AGG GAC ATC CTG CCG GAC TAT GAG CTC AAG CTC	432
15	Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu	
	130 135 140	
	ATC CAC CAC GAC AGC AAG TGT GAT CCA GGC CAA GCC ACC AAG TAC CTA	480
	Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu	
20	145 150 155 160	
	TAT GAG CTG CTC TAC AAC GAC CCT ATC AAG ATC ATC CTT ATG CCT GGC	528
	Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly	
	165 170 175	
25	TGC AGC TCT GTC TCC ACG CTG GTG GCT GAG GCT GCT AGG ATG TGG AAC	576
	Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn	
	180 185 190	
30	CTC ATT GTG CTT TCC TAT GGC TCC AGC TCA CCA GCC CTG TCA AAC CGG	624
	Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg	
	195 200 205	
	CAG CGT TTC CCC ACT TTC TTC CGA ACG CAC CCA TCA GCC ACA CTC CAC	672
35	Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His	
	210 215 220	
	AAC CCT ACC CGC GTG AAA CTC TTT GAA AAG TGG GGC TGG AAG AAG ATT	720
	Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile	
40	225 230 235 240	
	GCT ACC ATC CAG CAG ACC ACT GAG GTC TTC ACT TCG ACT CTG GAC GAC	768
	Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp	

	245	250	255	
	CTG GAG GAA CGA GTG AAG GAG GCT GGA ATT GAG ATT ACT TTC CGC CAG	816		
	Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln			
5	260	265	270	
	AGT TTC TTC TCA GAT CCA GCT GTG CCC GTC AAA AAC CTG AAG CGC CAG	864		
	Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln			
	275	280	285	
10	GAT GCC CGA ATC ATC GTG GGA CTT TTC TAT GAG ACT GAA GCC CGG AAA	912		
	Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys			
	290	295	300	
15	GTT TTT TGT GAG GTG TAC AAG GAG CGT CTC TTT GGG AAG AAG TAC GTC	960		
	Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val			
	305	310	315	320
	TGG TTC CTC ATT GGG TGG TAT GCT GAC AAT TGG TTC AAG ATC TAC GAC	1008		
20	Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp			
	325	330	335	
	CCT TCT ATC AAC TGC ACA GTG GAT GAG ATG ACT GAG GCG GTG GAG GGC	1056		
	Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly			
25	340	345	350	
	CAC ATC ACA ACT GAG ATT GTC ATG CTG AAT CCT GCC AAT ACC CGC AGC	1104		
	His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser			
	355	360	365	
30	ATT TCC AAC ATG ACA TCC CAG GAA TTT GTG GAG AAA CTA ACC AAG CGA	1152		
	Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg			
	370	375	380	
35	CTG AAA AGA CAC CCT GAG GAG ACA GGA GGC TTC CAG GAG GCA CCG CTG	1200		
	Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu			
	385	390	395	400
	GCC TAT GAT GCC ATC TGG GCC TTG GCA CTG GCC CTG AAC AAG ACA TCT	1248		
40	Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser			
	405	410	415	
	GGA GGA GGC GGC CGT TCT GGT GTG CGC CTG GAG GAC TTC AAC TAC AAC	1296		

	Gly	Gly	Gly	Gly	Arg	Ser	Gly	Val	Arg	Leu	Glu	Asp	Phe	Asn	Tyr	Asn	
				420					425					430			
	AAC	CAG	ACC	ATT	ACC	GAC	CAA	ATC	TAC	CGG	GCA	ATG	AAC	TCT	TCG	TCC	1344
5	Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	Arg	Ala	Met	Asn	Ser	Ser	Ser	
			435					440					445				
	TTT	GAG	GGT	GTC	TCT	GGC	CAT	GTG	GTG	TTT	GAT	GCC	AGC	GGC	TCT	CGG	1392
	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp	Ala	Ser	Gly	Ser	Arg	
10		450					455				460						
	ATG	GCA	TGG	ACG	CTT	ATC	GAG	CAG	CTT	CAG	GGT	GGC	AGC	TAC	AAG	AAG	1440
	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	Gln	Gly	Gly	Ser	Tyr	Lys	Lys	
	465					470				475						480	
15																	
	ATT	GGC	TAC	TAT	GAC	AGC	ACC	AAG	GAT	GAT	CTT	TCC	TGG	TCC	AAA	ACA	1488
	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	Asp	Leu	Ser	Trp	Ser	Lys	Thr	
					485					490					495		
	GAT	AAA	TGG	ATT	GGA	GGG	TCC	CCC	CCA	GCT	GAC	CAG	ACC	CTG	GTC	ATC	1536
20	Asp	Lys	Trp	Ile	Gly	Gly	Ser	Pro	Pro	Ala	Asp	Gln	Thr	Leu	Val	Ile	
				500					505					510			
	AAG	ACA	TTC	CGC	TTC	CTG	TCA	CAG	AAA	CTC	TTT	ATC	TCC	GTC	TCA	GTT	1584
25	Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys	Leu	Phe	Ile	Ser	Val	Ser	Val	
			515					520					525				
	CTC	TCC	AGC	CTG	GGC	ATT	GTC	CTA	GCT	GTT	GTC	TGT	CTG	TCC	TTT	AAC	1632
	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	Val	Val	Cys	Leu	Ser	Phe	Asn	
30		530					535					540					
	ATC	TAC	AAC	TCA	CAT	GTC	CGT	TAT	ATC	CAG	AAC	TCA	CAG	CCC	AAC	CTG	1680
	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	Gln	Asn	Ser	Gln	Pro	Asn	Leu	
	545					550				555					560		
35																	
	AAC	AAC	CTG	ACT	GCT	GTG	GGC	TGC	TCA	CTG	GCT	TTA	GCT	GCT	GTC	TTC	1728
	Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	Leu	Ala	Leu	Ala	Ala	Val	Phe	
					565					570					575		
	CCC	CTG	GGG	CTC	GAT	GGT	TAC	CAC	ATT	GGG	AGG	AAC	CAG	TTT	CCT	TTC	1776
40	Pro	Leu	Gly	Leu	Asp	Gly	Tyr	His	Ile	Gly	Arg	Asn	Gln	Phe	Pro	Phe	
				580					585					590			

	GTC TGC CAG GCC CGC CTC TGG CTC CTG GGC CTG GGC TTT AGT CTG GGC	1824
	Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly	
	595 600 605	
5	TAC GGT TCC ATG TTC ACC AAG ATT TGG TGG GTC CAC ACG GTC TTC ACA	1872
	Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr	
	610 615 620	
	AAG AAG GAA GAA AAG AAG GAG TGG AGG AAG ACT CTG GAA CCC TGG AAG	1920
10	Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys	
	625 630 635 640	
	CTG TAT GCC ACA GTG GGC CTG CTG GTG GGC ATG GAT GTC CTC ACT CTC	1968
	Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu	
15	645 650 655	
	GCC ATC TGG CAG ATC GTG GAC CCT CTG CAC CGG ACC ATT GAG ACA TTT	2016
	Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe	
	660 665 670	
20	GCC AAG GAG GAA CCT AAG GAA GAT ATT GAC GTC TCT ATT CTG CCC CAG	2064
	Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln	
	675 680 685	
25	CTG GAG CAT TGC AGC TCC AGG AAG ATG AAT ACA TGG CTT GGC ATT TTC	2112
	Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr Trp Leu Gly Ile Phe	
	690 695 700	
	TAT GGT TAC AAG GGG CTG CTG CTG CTG CTG GGA ATC TTC CTT GCT TAT	2160
30	Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr	
	705 710 715 720	
	GAG ACC AAG AGT GTG TCC ACT GAG AAG ATC AAT GAT CAC CGG GCT GTG	2208
	Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val	
35	725 730 735	
	GGC ATG GCT ATC TAC AAT GTG GCA GTC CTG TGC CTC ATC ACT GCT CCT	2256
	Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro	
	740 745 750	
40	GTC ACC ATG ATT CTG TCC AGC CAG CAG GAT GCA GCC TTT GCC TTT GCC	2304
	Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala	
	755 760 765	

TCT CTT GCC ATA GTT TTC TCC TCC TAT ATC ACT CTT GTT GTG CTC TTT 2352
 Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe
 770 775 780

5

GTG CCC AAG ATG CGC AGG CTG ATC ACC CGA GGG GAA TGG CAG TCG GAG 2400
 Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu
 785 790 795 800

10

GCG CAG GAC ACC ATG AAG ACA GGG TCA TCG ACC AAC AAC AAC GAG GAG 2448
 Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu
 805 810 815

15

GAG AAG TCC CGG CTG TTG GAG AAG GAG AAC CGT GAA CTG GAA AAG ATC 2496
 Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile
 820 825 830

20

ATT GCT GAG AAA GAG GAG CGT GTC TCT GAA CTG CGC CAT CAA CTC CAG 2544
 Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln
 835 840 845

25

TCT CGG CAG CAG CTC CGC TCC CGG CGC CAC CCA CCG ACA CCC CCA GAA 2592
 Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu
 850 855 860

CCC TCT GGG GGC CTG CCC AGG GGA CCC CCT GAG CCC CCC GAC CGG CTT 2640
 Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu
 865 870 875 880

30

AGC TGT GAT GGG AGT CGA GTG CAT TTG CTT TAT AAG TGA 2679
 Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys *
 885 890

35 (2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 892 amino acids

(B) TYPE: amino acid

40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 1 5 10 15
 5
 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 20 25 30
 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 10 35 40 45
 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
 50 55 60
 15 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
 65 70 75 80
 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
 85 90 95
 20 Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly
 100 105 110
 Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu
 25 115 120 125
 Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu
 130 135 140
 30 Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu
 145 150 155 160
 Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly
 165 170 175
 35 Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn
 180 185 190
 Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg
 40 195 200 205
 Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His
 210 215 220

Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile
 225 230 235 240

5 Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp
 245 250 255

Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln
 260 265 270

10 Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln
 275 280 285

Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys
 15 290 295 300

Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val
 305 310 315 320

20 Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp
 325 330 335

Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly
 340 345 350

25 His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser
 355 360 365

Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg
 30 370 375 380

Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu
 385 390 395 400

35 Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser
 405 410 415

Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn
 420 425 430

40 Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser
 435 440 445

Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg
 450 455 460

Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys
 5 465 470 475 480

Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr
 485 490 495

10 Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp Gln Thr Leu Val Ile
 500 505 510

Lys Thr Phe Arg Phe Leu Ser Gln Lys Leu Phe Ile Ser Val Ser Val
 515 520 525

15 Leu Ser Ser Leu Gly Ile Val Leu Ala Val Val Cys Leu Ser Phe Asn
 530 535 540

Ile Tyr Asn Ser His Val Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu
 20 545 550 555 560

Asn Asn Leu Thr Ala Val Gly Cys Ser Leu Ala Leu Ala Ala Val Phe
 565 570 575

25 Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Asn Gln Phe Pro Phe
 580 585 590

Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly
 595 600 605

30 Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr
 610 615 620

Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys
 35 625 630 635 640

Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu
 645 650 655

40 Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe
 660 665 670

Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln

	675		680		685	
	Leu Glu His Cys Ser Ser Arg Lys Met Asn Thr Trp Leu Gly Ile Phe					
	690		695		700	
5	Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr					
	705		710		715	720
	Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val					
10		725		730		735
	Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro					
		740		745		750
15	Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala					
		755		760		765
	Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe					
		770		775		780
20	Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu					
		785		790		800
	Ala Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu					
25		805		810		815
	Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile					
		820		825		830
30	Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln					
		835		840		845
	Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu					
		850		855		860
35	Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu					
		865		870		875
	Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr Lys					
40		885		890		

(2) INFORMATION FOR SEQ ID NO: 76:

H1865-1 WO SEQ

145

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2661 base pairs

(B) TYPE: nucleic acid

5 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

10 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

15 (A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..2661

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC 48
 Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 25 1 5 10 15

GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC 96
 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 20 25 30

30

ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG 144
 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 35 40 45

35 GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG 192
 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
 50 55 60

40 TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG 240
 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
 65 70 75 80

TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT 288

	Cys	Leu	Ala	Asn	Gly	Ser	Trp	Thr	Asp	Met	Asp	Thr	Pro	Ser	Arg	Cys	
					85					90						95	
	GTG	AAT	CGA	ACG	CCA	CAC	TCA	GAA	CGG	CGC	GCA	GTG	TAC	ATC	GGG	GCA	336
5	Val	Asn	Arg	Thr	Pro	His	Ser	Glu	Arg	Arg	Ala	Val	Tyr	Ile	Gly	Ala	
				100					105					110			
	CTG	TTT	CCC	GCG	GTG	GAG	ATG	GCG	CTG	GAG	GAC	GTG	AAT	AGC	CGC	AGG	384
10	Leu	Phe	Pro	Ala	Val	Glu	Met	Ala	Leu	Glu	Asp	Val	Asn	Ser	Arg	Arg	
			115					120					125				
	GAC	ATC	CTG	CCG	GAC	TAT	GAG	CTC	AAG	CTC	ATC	CAC	CAC	GAC	AGC	AAG	432
	Asp	Ile	Leu	Pro	Asp	Tyr	Glu	Leu	Lys	Leu	Ile	His	His	Asp	Ser	Lys	
		130					135				140						
15	TGT	GAT	CCA	GGC	CAA	GCC	ACC	AAG	TAC	CTA	TAT	GAG	CTG	CTC	TAC	AAC	480
	Cys	Asp	Pro	Gly	Gln	Ala	Thr	Lys	Tyr	Leu	Tyr	Glu	Leu	Leu	Tyr	Asn	
	145				150					155						160	
20	GAC	CCT	ATC	AAG	ATC	ATC	CTT	ATG	CCT	GGC	TGC	AGC	TCT	GTC	TCC	ACG	528
	Asp	Pro	Ile	Lys	Ile	Ile	Leu	Met	Pro	Gly	Cys	Ser	Ser	Val	Ser	Thr	
				165					170					175			
	CTG	GTG	GCT	GAG	GCT	GCT	AGG	ATG	TGG	AAC	CTC	ATT	GTG	CTT	TCC	TAT	576
25	Leu	Val	Ala	Glu	Ala	Ala	Arg	Met	Trp	Asn	Leu	Ile	Val	Leu	Ser	Tyr	
			180					185					190				
	GGC	TCC	AGC	TCA	CCA	GCC	CTG	TCA	AAC	CGG	CAG	CGT	TTC	CCC	ACT	TTC	624
30	Gly	Ser	Ser	Ser	Pro	Ala	Leu	Ser	Asn	Arg	Gln	Arg	Phe	Pro	Thr	Phe	
			195				200						205				
	TTC	CGA	ACG	CAC	CCA	TCA	GCC	ACA	CTC	CAC	AAC	CCT	ACC	CGC	GTG	AAA	672
	Phe	Arg	Thr	His	Pro	Ser	Ala	Thr	Leu	His	Asn	Pro	Thr	Arg	Val	Lys	
		210					215					220					
35	CTC	TTT	GAA	AAG	TGG	GGC	TGG	AAG	AAG	ATT	GCT	ACC	ATC	CAG	CAG	ACC	720
	Leu	Phe	Glu	Lys	Trp	Gly	Trp	Lys	Lys	Ile	Ala	Thr	Ile	Gln	Gln	Thr	
	225				230					235					240		
40	ACT	GAG	GTC	TTC	ACT	TCG	ACT	CTG	GAC	GAC	CTG	GAG	GAA	CGA	GTG	AAG	768
	Thr	Glu	Val	Phe	Thr	Ser	Thr	Leu	Asp	Asp	Leu	Glu	Glu	Arg	Val	Lys	
				245					250					255			

	GAG GCT GGA ATT GAG ATT ACT TTC CGC CAG AGT TTC TTC TCA GAT CCA	816
	Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro	
	260 265 270	
5	GCT GTG CCC GTC AAA AAC CTG AAG CGC CAG GAT GCC CGA ATC ATC GTG	864
	Ala Val Pro Val Lys Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val	
	275 280 285	
10	GGA CTT TTC TAT GAG ACT GAA GCC CGG AAA GTT TTT TGT GAG GTG TAC	912
	Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr	
	290 295 300	
15	AAG GAG CGT CTC TTT GGG AAG AAG TAC GTC TGG TTC CTC ATT GGG TGG	960
	Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp	
	305 310 315 320	
20	TAT GCT GAC AAT TGG TTC AAG ATC TAC GAC CCT TCT ATC AAC TGC ACA	1008
	Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr	
	325 330 335	
	GTG GAT GAG ATG ACT GAG GCG GTG GAG GGC CAC ATC ACA ACT GAG ATT	1056
	Val Asp Glu Met Thr Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile	
	340 345 350	
25	GTC ATG CTG AAT CCT GCC AAT ACC CGC AGC ATT TCC AAC ATG ACA TCC	1104
	Val Met Leu Asn Pro Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser	
	355 360 365	
30	CAG GAA TTT GTG GAG AAA CTA ACC AAG CGA CTG AAA AGA CAC CCT GAG	1152
	Gln Glu Phe Val Glu Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu	
	370 375 380	
35	GAG ACA GGA GGC TTC CAG GAG GCA CCG CTG GCC TAT GAT GCC ATC TGG	1200
	Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp	
	385 390 395 400	
40	GCC TTG GCA CTG GCC CTG AAC AAG ACA TCT GGA GGA GGC GGC CGT TCT	1248
	Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser	
	405 410 415	
	GGT GTG CGC CTG GAG GAC TTC AAC TAC AAC AAC CAG ACC ATT ACC GAC	1296
	Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp	
	420 425 430	

	CAA ATC TAC CGG GCA ATG AAC TCT TCG TCC TTT GAG GGT GTC TCT GGC	1344
	Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly	
	435 440 445	
5	CAT GTG GTG TTT GAT GCC AGC GGC TCT CGG ATG GCA TGG ACG CTT ATC	1392
	His Val Val Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile	
	450 455 460	
10	GAG CAG CTT CAG GGT GGC AGC TAC AAG AAG ATT GGC TAC TAT GAC AGC	1440
	Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser	
	465 470 475 480	
15	ACC AAG GAT GAT CTT TCC TGG TCC AAA ACA GAT AAA TGG ATT GGA GGC	1488
	Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly	
	485 490 495	
20	TCC CCC CCA GCT GAC CAG ACC CTG GTC ATC AAG ACA TTC CGC TTC CTG	1536
	Ser Pro Pro Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu	
	500 505 510	
25	TCA CAG AAA CTC TTT ATC TCC GTC TCA GTT CTC TCC AGC CTG GGC ATT	1584
	Ser Gln Lys Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile	
	515 520 525	
30	GTC CTA GCT GTT GTC TGT CTG TCC TTT AAC ATC TAC AAC TCA CAT GTC	1632
	Val Leu Ala Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val	
	530 535 540	
35	CGT TAT ATC CAG AAC TCA CAG CCC AAC CTG AAC AAC CTG ACT GCT GTG	1680
	Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val	
	545 550 555 560	
40	GGC TGC TCA CTG GCT TTA GCT GCT GTC TTC CCC CTG GGG CTC GAT GGT	1728
	Gly Cys Ser Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly	
	565 570 575	
45	TAC CAC ATT GGG AGG AAC CAG TTT CCT TTC GTC TGC CAG GCC CGC CTC	1776
	Tyr His Ile Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu	
	580 585 590	
50	TGG CTC CTG GGC CTG GGC TTT AGT CTG GGC TAC GGT TCC ATG TTC ACC	1824
	Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr	

	595	600	605	
5	AAG ATT TGG TGG GTC CAC ACG GTC TTC ACA AAG AAG GAA GAA AAG AAG Lys Ile Trp Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys	610	615	620
10	GAG TGG AGG AAG ACT CTG GAA CCC TGG AAG CTG TAT GCC ACA GTG GGC Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly	625	630	635
15	CTG CTG GTG GGC ATG GAT GTC CTC ACT CTC GCC ATC TGG CAG ATC GTG Leu Leu Val Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val	645	650	655
20	GAC CCT CTG CAC CGG ACC ATT GAG ACA TTT GCC AAG GAG GAA CCT AAG Asp Pro Leu His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys	660	665	670
25	GAA GAT ATT GAC GTC TCT ATT CTG CCC CAG CTG GAG CAT TGC AGC TCC Glu Asp Ile Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser	675	680	685
30	AGG AAG ATG AAT ACA TGG CTT GGC ATT TTC TAT GGT TAC AAG GGG CTG Arg Lys Met Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu	690	695	700
35	CTG CTG CTG CTG GGA ATC TTC CTT GCT TAT GAG ACC AAG AGT GTG TCC Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser	705	710	715
40	ACT GAG AAG ATC AAT GAT CAC CGG GCT GTG GGC ATG GCT ATC TAC AAT Thr Glu Lys Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn	725	730	735
45	GTG GCA GTC CTG TGC CTC ATC ACT GCT CCT GTC ACC ATG ATT CTG TCC Val Ala Val Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser	740	745	750
50	AGC CAG CAG GAT GCA GCC TTT GCC TTT GCC TCT CTT GCC ATA GTT TTC Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe	755	760	765
55	TCC TCC TAT ATC ACT CTT GTT GTG CTC TTT GTG CCC AAG ATG CGC AGG			

	Ser Ser Tyr Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg	
	770 775 780	
5	CTG ATC ACC CGA GGG GAA TGG CAG TCG GAG GCG CAG GAC ACC ATG AAG Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys	2400
	785 790 795 800	
10	ACA GGG TCA TCG ACC AAC AAC AAC GAG GAG GAG AAG TCC CGG CTG TTG Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu	2448
	805 810 815	
15	GAG AAG GAG AAC CGT GAA CTG GAA AAG ATC ATT GCT GAG AAA GAG GAG Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu	2496
	820 825 830	
20	CGT GTC TCT GAA CTG CGC CAT CAA CTC CAG TCT CGG CAG CAG CTC CGC Arg Val Ser Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg	2544
	835 840 845	
25	TCC CGG CGC CAC CCA CCG ACA CCC CCA GAA CCC TCT GGG GGC CTG CCC Ser Arg Arg His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro	2592
	850 855 860	
30	AGG GGA CCC CCT GAG CCC CCC GAC CGG CTT AGC TGT GAT GGG AGT CGA Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg	2640
	865 870 875 880	
35	GTG CAT TTG CTT TAT AAG TGA Val His Leu Leu Tyr Lys *	2661
	885	

(2) INFORMATION FOR SEQ ID NO: 77:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 886 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- 40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 1 5 10 15

Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 5 20 25 30

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 35 40 45

10 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
 50 55 60

Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
 65 70 75 80

15 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
 85 90 95

Val Asn Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala
 20 100 105 110

Leu Phe Pro Ala Val Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg
 115 120 125

25 Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys
 130 135 140

Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn
 145 150 155 160

30 Asp Pro Ile Lys Ile Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr
 165 170 175

Leu Val Ala Glu Ala Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr
 35 180 185 190

Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe
 195 200 205

40 Phe Arg Thr His Pro Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys
 210 215 220

Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr

Glu Gln Leu Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser
 465 470 475 480

5 Thr Lys Asp Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly
 485 490 495

Ser Pro Pro Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu
 500 505 510

10 Ser Gln Lys Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile
 515 520 525

Val Leu Ala Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val
 15 530 535 540

Arg Tyr Ile Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val
 545 550 555 560

20 Gly Cys Ser Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly
 565 570 575

Tyr His Ile Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu
 580 585 590

25 Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr
 595 600 605

Lys Ile Trp Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys
 30 610 615 620

Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly
 625 630 635 640

35 Leu Leu Val Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val
 645 650 655

Asp Pro Leu His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys
 660 665 670

40 Glu Asp Ile Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser
 675 680 685

Arg Lys Met Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu
 690 695 700

Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser
 5 705 710 715 720

Thr Glu Lys Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn
 725 730 735

10 Val Ala Val Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser
 740 745 750

Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe
 755 760 765

15 Ser Ser Tyr Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg
 770 775 780

Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys
 20 785 790 795 800

Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu
 805 810 815

25 Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu
 820 825 830

Arg Val Ser Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg
 835 840 845

30 Ser Arg Arg His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro
 850 855 860

Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg
 35 865 870 875 880

Val His Leu Leu Tyr Lys
 885

40

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

15

(B) LOCATION:1..1692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

20	ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
	Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
	1 5 10 15	
25	GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
	20 25 30	
30	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
	35 40 45	
35	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
	50 55 60	
40	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
	65 70 75 80	
	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	
	85 90 95	
	GTC CGA ATC TGC TCC AAG TCT TAT TTG ACC ATT ACC GAC CAA ATC TAC	336

	Val	Arg	Ile	Cys	Ser	Lys	Ser	Tyr	Leu	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	
				100					105					110			
	CGG	GCA	ATG	AAC	TCT	TCG	TCC	TTT	GAG	GGT	GTC	TCT	GGC	CAT	GTG	GTG	384
5	Arg	Ala	Met	Asn	Ser	Ser	Ser	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	
			115					120					125				
	TTT	GAT	GCC	AGC	GGC	TCT	CGG	ATG	GCA	TGG	ACG	CTT	ATC	GAG	CAG	CTT	432
	Phe	Asp	Ala	Ser	Gly	Ser	Arg	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	
10		130					135					140					
	CAG	GGT	GGC	AGC	TAC	AAG	AAG	ATT	GGC	TAC	TAT	GAC	AGC	ACC	AAG	GAT	480
	Gln	Gly	Gly	Ser	Tyr	Lys	Lys	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	
	145					150					155				160		
15	GAT	CTT	TCC	TGG	TCC	AAA	ACA	GAT	AAA	TGG	ATT	GGA	GGG	TCC	CCC	CCA	528
	Asp	Leu	Ser	Trp	Ser	Lys	Thr	Asp	Lys	Trp	Ile	Gly	Gly	Ser	Pro	Pro	
					165					170					175		
20	GCT	GAC	CAG	ACC	CTG	GTC	ATC	AAG	ACA	TTC	CGC	TTC	CTG	TCA	CAG	AAA	576
	Ala	Asp	Gln	Thr	Leu	Val	Ile	Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys	
				180					185					190			
	CTC	TTT	ATC	TCC	GTC	TCA	GTT	CTC	TCC	AGC	CTG	GGC	ATT	GTC	CTA	GCT	624
25	Leu	Phe	Ile	Ser	Val	Ser	Val	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	
			195					200					205				
	GTT	GTC	TGT	CTG	TCC	TTT	AAC	ATC	TAC	AAC	TCA	CAT	GTC	CGT	TAT	ATC	672
	Val	Val	Cys	Leu	Ser	Phe	Asn	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	
30		210					215					220					
	CAG	AAC	TCA	CAG	CCC	AAC	CTG	AAC	AAC	CTG	ACT	GCT	GTG	GGC	TGC	TCA	720
	Gln	Asn	Ser	Gln	Pro	Asn	Leu	Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	
	225					230					235				240		
35	CTG	GCT	TTA	GCT	GCT	GTC	TTC	CCC	CTG	GGG	CTC	GAT	GGT	TAC	CAC	ATT	768
	Leu	Ala	Leu	Ala	Ala	Val	Phe	Pro	Leu	Gly	Leu	Asp	Gly	Tyr	His	Ile	
					245					250				255			
40	GGG	AGG	AAC	CAG	TTT	CCT	TTC	GTC	TGC	CAG	GCC	CGC	CTC	TGG	CTC	CTG	816
	Gly	Arg	Asn	Gln	Phe	Pro	Phe	Val	Cys	Gln	Ala	Arg	Leu	Trp	Leu	Leu	
				260					265					270			

	GGC CTG GGC TTT AGT CTG GGC TAC GGT TCC ATG TTC ACC AAG ATT TGG	864
	Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp	
	275 280 285	
5	TGG GTC CAC ACG GTC TTC ACA AAG AAG GAA GAA AAG AAG GAG TGG AGG	912
	Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg	
	290 295 300	
	AAG ACT CTG GAA CCC TGG AAG CTG TAT GCC ACA GTG GGC CTG CTG GTG	960
10	Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val	
	305 310 315 320	
	GGC ATG GAT GTC CTC ACT CTC GCC ATC TGG CAG ATC GTG GAC CCT CTG	1008
15	Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu	
	325 330 335	
	CAC CGG ACC ATT GAG ACA TTT GCC AAG GAG GAA CCT AAG GAA GAT ATT	1056
	His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile	
	340 345 350	
20	GAC GTC TCT ATT CTG CCC CAG CTG GAG CAT TGC AGC TCC AGG AAG ATG	1104
	Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met	
	355 360 365	
25	AAT ACA TGG CTT GGC ATT TTC TAT GGT TAC AAG GGG CTG CTG CTG CTG	1152
	Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu	
	370 375 380	
	CTG GGA ATC TTC CTT GCT TAT GAG ACC AAG AGT GTG TCC ACT GAG AAG	1200
30	Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys	
	385 390 395 400	
	ATC AAT GAT CAC CGG GCT GTG GGC ATG GCT ATC TAC AAT GTG GCA GTC	1248
35	Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val	
	405 410 415	
	CTG TGC CTC ATC ACT GCT CCT GTC ACC ATG ATT CTG TCC AGC CAG CAG	1296
	Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln	
	420 425 430	
40	GAT GCA GCC TTT GCC TTT GCC TCT CTT GCC ATA GTT TTC TCC TCC TAT	1344
	Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr	
	435 440 445	

ATC ACT CTT GTT GTG CTC TTT GTG CCC AAG ATG CGC AGG CTG ATC ACC 1392
 Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr
 450 455 460

5 CGA GGG GAA TGG CAG TCG GAG GCG CAG GAC ACC ATG AAG ACA GGG TCA 1440
 Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser
 465 470 475 480

10 TCG ACC AAC AAC AAC GAG GAG GAG AAG TCC CGG CTG TTG GAG AAG GAG 1488
 Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu
 485 490 495

15 AAC CGT GAA CTG GAA AAG ATC ATT GCT GAG AAA GAG GAG CGT GTC TCT 1536
 Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser
 500 505 510

20 GAA CTG CGC CAT CAA CTC CAG TCT CGG CAG CAG CTC CGC TCC CGG CGC 1584
 Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg
 515 520 525

CAC CCA CCG ACA CCC CCA GAA CCC TCT GGG GGC CTG CCC AGG GGA CCC 1632
 His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro
 530 535 540

25 CCT GAG CCC CCC GAC CGG CTT AGC TGT GAT GGG AGT CGA GTG CAT TTG 1680
 Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu
 545 550 555 560

30 CTT TAT AAG TGA 1692
 Leu Tyr Lys *

35 (2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 563 amino acids

(B) TYPE: amino acid

40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 1 5 10 15
 5
 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 20 25 30
 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 10 35 40 45
 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
 50 55 60
 15 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
 65 70 75 80
 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
 85 90 95
 20 Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Ile Thr Asp Gln Ile Tyr
 100 105 110
 Arg Ala Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val
 25 115 120 125
 Phe Asp Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu
 130 135 140
 30 Gln Gly Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp
 145 150 155 160
 Asp Leu Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro
 165 170 175
 35 Ala Asp Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys
 180 185 190
 Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala
 40 195 200 205
 Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile
 210 215 220

Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser
 225 230 235 240

5 Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile
 245 250 255

Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu
 260 265 270

10 Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp
 275 280 285

Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg
 15 290 295 300

Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val
 305 310 315 320

20 Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu
 325 330 335

His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile
 340 345 350

25 Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met
 355 360 365

Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu
 30 370 375 380

Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys
 385 390 395 400

35 Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val
 405 410 415

Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln
 420 425 430

40 Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr
 435 440 445

Ile Thr Leu Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr
450 455 460

Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr Met Lys Thr Gly Ser
5 465 470 475 480

Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg Leu Leu Glu Lys Glu
485 490 495

10 Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys Glu Glu Arg Val Ser
500 505 510

Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln Leu Arg Ser Arg Arg
515 520 525

15 His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro
530 535 540

Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu
20 545 550 555 560

Leu Tyr Lys

25

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 2602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

35

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

40

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

	ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
5	Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
	1 5 10 15	
	GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
10	20 25 30	
	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
	35 40 45	
15	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAT	192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Asp	
	50 55 60	
20	GAA TCG AAC GCC ACA CTC AGA ACG GCG CGC AGT GTA CAT CGG GGC ACT	240
	Glu Ser Asn Ala Thr Leu Arg Thr Ala Arg Ser Val His Arg Gly Thr	
	65 70 75 80	
	GTT TCC CAT GAG CGG GGG CTG GCC AGG GGG CCA GGC CTG CCA GCC CGC	288
25	Val Ser His Glu Arg Gly Leu Ala Arg Gly Pro Gly Leu Pro Ala Arg	
	85 90 95	
	GGT GGA GAT GGC GCT GGA GGA CGT GAA TAG CCGCAGGGAC ATCCTGCCGG	338
	Gly Gly Asp Gly Ala Gly Gly Arg Glu *	
30	100 105	
	ACTATGAGCT CAAGCTCATC CACCACGACA GCAAGTGTGA TCCAGGCCAA GCCACCAAGT	398
	ACCTATATGA GCTGCTCTAC AACGACCCTA TCAAGATCAT CCTTATGCCT GGCTGCAGCT	458
35	CTGTCTCCAC GCTGGTGGCT GAGGCTGCTA GGATGTGGAA CCTCATTGTG CTTTCCTATG	518
	GCTCCAGCTC ACCAGCCCTG TCAAACCGGC AGCGTTTCCC CACTTTCTTC CGAACGCACC	578
40	CATCAGCCAC ACTCCACAAC CCTACCCGCG TGAAACTCTT TGAAAAGTGG GGCTGGAAGA	638
	AGATTGCTAC CATCCAGCAG ACCACTGAGG TCTTCACTTC GACTCTGGAC GACCTGGAGG	698

	AACGAGTGAA GGAGGCTGGA ATTGAGATTA CTTTCCGCCA GAGTTTCTTC TCAGATCCAG	758
	CTGTGCCCCGT CAAAAACCTG AAGCGCCAGG ATGCCCGAAT CATCGTGGGA CTTTTCTATG	818
5	AGACTGAAGC CCGGAAAGTT TTTTGTGAGG TGTACAAGGA GCGTCTCTTT GGGAAGAAGT	878
	ACGTCTGGTT CCTCATTGGG TGGTATGCTG ACAATTGGTT CAAGATCTAC GACCCTTCTA	938
	TCAACTGCAC AGTGGATGAG ATGACTGAGG CGGTGGAGGG CCACATCACA ACTGAGATTG	998
10	TCATGCTGAA TCCTGCCAAT ACCCGCAGCA TTTCCAACAT GACATCCCAG GAATTTGTGG	1058
	AGAAACTAAC CAAGCGACTG AAAAGACACC CTGAGGAGAC AGGAGGCTTC CAGGAGGCAC	1118
15	CGCTGGCCTA TGATGCCATC TGGGCCTTGG CACTGGCCCT GAACAAGACA TCTGGAGGAG	1178
	GCGGCCGTTT TGGTGTGCGC CTGGAGGACT TCAACTACAA CAACCAGACC ATTACCGACC	1238
	AAATCTACCG GGCAATGAAC TCTTCGTCTT TTAGGGTGT CTCTGGCCAT GTGGTGTTTG	1298
20	ATGCCAGCGG CTCTCGGATG GCATGGACGC TTATCGAGCA GCTTCAGGGT GGCAGCTACA	1358
	AGAAGATTGG CTACTATGAC AGCACCAAGG ATGATCTTTC CTGGTCCAAA ACAGATAAAT	1418
25	GGATTGGAGG GTCCCCCCA GCTGACCAGA CCCTGGTCAT CAAGACATTC CGCTTCCTGT	1478
	CACAGAACT CTTTATCTCC GTCTCAGTTC TCTCCAGCCT GGGCATTGTC CTAGCTGTTG	1538
	TCTGTCTGTC CTTTAACATC TACAACTCAC ATGTCCGTTA TATCCAGAAC TCACAGCCCA	1598
30	ACCTGAACAA CCTGACTGCT GTGGGCTGCT CACTGGCTTT AGCTGCTGTC TTCCCCCTGG	1658
	GGCTCGATGG TTACCACATT GGGAGGAACC AGTTTCCTTT CGTCTGCCAG GCCCGCCTCT	1718
35	GGCTCCTGGG CCTGGGCTTT AGTCTGGGCT ACGGTTCCAT GTTCACCAAG ATTTGGTGGG	1778
	TCCACACGGT CTTCAAAAG AAGGAAGAAA AGAAGGAGTG GAGGAAGACT CTGGAACCCT	1838
	GGAAGCTGTA TGCCACAGTG GGCCTGCTGG TGGGCATGGA TGTCCCTCACT CTCGCCATCT	1898
40	GGCAGATCGT GGACCCTCTG CACCGGACCA TTGAGACATT TGCCAAGGAG GAACCTAAGG	1958
	AAGATATTGA CGTCTCTATT CTGCCCCAGC TGGAGCATTG CAGCTCCAGG AAGATGAATA	2018

CATGGCTTGG CATTCTCTAT GGTTACAAGG GGCTGCTGCT GCTGCTGGGA ATCTTCCTTG 2078
 CTTATGAGAC CAAGAGTGTG TCCACTGAGA AGATCAATGA TCACCGGGCT GTGGGCATGG 2138
 5 CTATCTACAA TGTGGCAGTC CTGTGCCTCA TCACTGCTCC TGTCACCATG ATTCTGTCCA 2198
 GCCAGCAGGA TGCAGCCTTT GCCTTTGCCT CTCTTGCCAT AGTTTTCTCC TCCTATATCA 2258
 10 CTCTTGTTGT GCTCTTTGTG CCAAGATGC GCAGGCTGAT CACCCGAGGG GAATGGCAGT 2318
 CGGAGGCGCA GGACACCATG AAGACAGGGT CATCGACCAA CAACAACGAG GAGGAGAAGT 2378
 CCCGGCTGTT GGAGAAGGAG AACCGTGAAC TGGAAAAGAT CATTGCTGAG AAAGAGGAGC 2438
 15 GTGTCTCTGA ACTGCGCCAT CAACTCCAGT CTCGGCAGCA GCTCCGCTCC CGGCGCCACC 2498
 CACCGACACC CCCAGAACCC TCTGGGGGCC TGCCCAGGGG ACCCCCTGAG CCCCCGACC 2558
 20 GGCTTAGCTG TGATGGGAGT CGAGTGCATT TGCTTTATAA GTGA 2602

(2) INFORMATION FOR SEQ ID NO: 81:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Met Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 35 1 5 10 15
 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 20 25 30
 40 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 35 40 45
 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Asp

50 55 60

Glu Ser Asn Ala Thr Leu Arg Thr Ala Arg Ser Val His Arg Gly Thr
 65 70 75 80

5 Val Ser His Glu Arg Gly Leu Ala Arg Gly Pro Gly Leu Pro Ala Arg
 85 90 95

Gly Gly Asp Gly Ala Gly Gly Arg Glu
 10 100 105

(2) INFORMATION FOR SEQ ID NO: 82:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(ix) FEATURE:
 (A) NAME/KEY: CDS
 30 (B) LOCATION: 1..294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC 48
 35 Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
 1 5 10 15

GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC 96
 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
 40 20 25 30

ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG 144
 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg

	35	40	45	
	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192		
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu			
5	50	55	60	
	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240		
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys			
	65	70	75	80
10	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288		
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys			
	85	90	95	
15	GTG TGA TCCAGGCCAA GCCACCAAGT ACCTATATGA GCTGCTCTAC AACGACCCTA	344		
	Val *			
	TCAAGATCAT CCTTATGCCT GGCTGCAGCT CTGTCTCCAC GCTGGTGGCT GAGGCTGCTA	404		
20	GGATGTGGAA CCTCATTGTG CTTTCCTATG GCTCCAGCTC ACCAGCCCTG TCAAACCGGC	464		
	AGCGTTTCCC CACTTTCTTC CGAACGCACC CATCAGCCAC ACTCCACAAC CCTACCCGCG	524		
25	TGAAACTCTT TGAAAAGTGG GGCTGGAAGA AGATTGCTAC CATCCAGCAG ACCACTGAGG	584		
	TCTTCACTTC GACTCTGGAC GACCTGGAGG AACGAGTGAA GGAGGCTGGA ATTGAGATTA	644		
	CTTTCCGCCA GAGTTTCTTC TCAGATCCAG CTGTGCCCCGT CAAAAACCTG AAGCGCCAGG	704		
30	ATGCCCCGAAT CATCGTGGGA CTTTTCTATG AGACTGAAGC CCGGAAAGTT TTTTGTGAGG	764		
	TGTACAAGGA GCGTCTCTTT GGGAAGAAGT ACGTCTGGTT CCTCATTGGG TGGTATGCTG	824		
35	ACAATTGGTT CAAGATCTAC GACCCTTCTA TCAACTGCAC AGTGGATGAG ATGACTGAGG	884		
	CGGTGGAGGG CCACATCACA ACTGAGATTG TCATGCTGAA TCCTGCCAAT ACCCGCAGCA	944		
	TTTCCAACAT GACATCCCAG GAATTTGTGG AGAACTAAC CAAGCGACTG AAAAGACACC	1004		
40	CTGAGGAGAC AGGAGGCTTC CAGGAGGCAC CGCTGGCCTA TGATGCCATC TGGGCCTTGG	1064		
	CACTGGCCCT GAACAAGACA TCTGGAGGAG GCGGCCGTTT TGGTGTGCGC CTGGAGGACT	1124		

	TCAACTACAA	CAACCAGACC	ATTACCGACC	AAATCTACCG	GGCAATGAAC	TCTTCGTCCT	1184
	TTGAGGGTGT	CTCTGGCCAT	GTGGTGTTTG	ATGCCAGCGG	CTCTCGGATG	GCATGGACGC	1244
5	TTATCGAGCA	GCTTCAGGGT	GGCAGCTACA	AGAAGATTGG	CTACTATGAC	AGCACCAAGG	1304
	ATGATCTTTC	CTGGTCCAAA	ACAGATAAAT	GGATTGTTAT	ATCCAGAACT	CACAGCCCCA	1364
10	CCTGAACAAC	CTGACTGCTG	TGGGCTGCTC	ACTGGCTTTA	GCTGCTGTCT	TCCCCCTGGG	1424
	GCTCGATGGT	TACCACATTG	GGAGGAACCA	GTTTCCTTTC	GTCTGCCAGG	CCCGCCTCTG	1484
	GCTCCTGGGC	CTGGGCTTTA	GTCTGGGCTA	CGGTTCCATG	TTCACCAAGA	TTTGGTGGGT	1544
15	CCACACGGTC	TTCACAAAGA	AGGAAGAAAA	GAAGGAGTGG	AGGAAGACTC	TGGAACCCTG	1604
	GAAGCTGTAT	GCCACAGTGG	GCCTGCTGGT	GGGCATGGAT	GTCTCACTC	TCGCCATCTG	1664
20	GCAGATCGTG	GACCCTCTGC	ACCGGACCAT	TGAGACATTT	GCCAAGGAGG	AACCTAAGGA	1724
	AGATATTGAC	GTCTCTATTC	TGCCCCAGCT	GGAGCATTGC	AGCTCCAGGA	AGATGAATAC	1784
	ATGGCTTGGC	ATTTTCTATG	GTTACAAGGG	GCTGCTGCTG	CTGCTGGGAA	TCTTCCTTGC	1844
25	TTATGAGACC	AAGAGTGTTG	CCACTGAGAA	GATCAATGAT	CACCGGGCTG	TGGGCATGGC	1904
	TATCTACAAT	GTGGCAGTCC	TGTGCCTCAT	CACTGCTCCT	GTCAACCATGA	TTCTGTCCAG	1964
30	CCAGCAGGAT	GCAGCCTTTG	CCTTTGCCTC	TCTTGCCATA	GTTTTCTCCT	CCTATATCAC	2024
	TCTTGTTGTG	CTCTTTGTGC	CCAAGATGCG	CAGGCTGATC	ACCCGAGGGG	AATGGCAGTC	2084
	GGAGGCCGAG	GACACCATGA	AGACAGGGTC	ATCGACCAAC	AACAACGAGG	AGGAGAAGTC	2144
35	CCGGCTGTTG	GAGAAGGAGA	ACCGTGAAC	GGAAAAGATC	ATTGCTGAGA	AAGAGGAGCG	2204
	TGTCTCTGAA	CTGCGCCATC	AACTCCAGTC	TCGGCAGCAG	CTCCGCTCCC	GGCGCCACCC	2264
40	ACCGACACCC	CCAGAACCCT	CTGGGGGCCT	GCCCAGGGGA	CCCCCTGAGC	CCCCCGACCG	2324
	GCTTAGCTGT	GATGGGAGTC	GAGTGCATTT	GCTTTATAAG	TGA		2367

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
1 5 10 15

Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
20 25 30

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
35 40 45

Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
50 55 60

Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
65 70 75 80

Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
85 90 95

Val

35 (2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2489 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

10

(A) NAME/KEY: CDS

(B) LOCATION:1..1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

15	ATG TTG CTG CTG CTG CTA CTG GCG CCA CTC TTC CTC CGC CCC CCG GGC	48
	Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly	
	1 5 10 15	
	GCG GGC GGG GCG CAG ACC CCC AAC GCC ACC TCA GAA GGT TGC CAG ATC	96
20	Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile	
	20 25 30	
	ATA CAC CCG CCC TGG GAA GGG GGC ATC AGG TAC CGG GGC CTG ACT CGG	144
	Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg	
25	35 40 45	
	GAC CAG GTG AAG GCT ATC AAC TTC CTG CCA GTG GAC TAT GAG ATT GAG	192
	Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu	
	50 55 60	
30	TAT GTG TGC CGG GGG GAG CGC GAG GTG GTG GGG CCC AAG GTC CGC AAG	240
	Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys	
	65 70 75 80	
35	TGC CTG GCC AAC GGC TCC TGG ACA GAT ATG GAC ACA CCC AGC CGC TGT	288
	Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys	
	85 90 95	
	GTC CGA ATC TGC TCC AAG TCT TAT TTG ACC CTG GAA AAT GGG AAG GTT	336
40	Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val	
	100 105 110	
	TTC CTG ACG GGT GGG GAC CTC CCA GCT CTG GAC GGA GCC CGG GTG GAT	384

	Phe	Leu	Thr	Gly	Gly	Asp	Leu	Pro	Ala	Leu	Asp	Gly	Ala	Arg	Val	Asp	
				115				120					125				
	TTC	CGG	TGT	GAC	CCC	GAC	TTC	CAT	CTG	TGT	GAT	CCA	GGC	CAA	GCC	ACC	432
5	Phe	Arg	Cys	Asp	Pro	Asp	Phe	His	Leu	Cys	Asp	Pro	Gly	Gln	Ala	Thr	
		130					135				140						
	AAG	TAC	CTA	TAT	GAG	CTG	CTC	TAC	AAC	GAC	CCT	ATC	AAG	ATC	ATC	CTT	480
	Lys	Tyr	Leu	Tyr	Glu	Leu	Leu	Tyr	Asn	Asp	Pro	Ile	Lys	Ile	Ile	Leu	
10	145					150					155				160		
	ATG	CCT	GGC	TGC	AGC	TCT	GTC	TCC	ACG	CTG	GTG	GCT	GAG	GCT	GCT	AGG	528
	Met	Pro	Gly	Cys	Ser	Ser	Val	Ser	Thr	Leu	Val	Ala	Glu	Ala	Ala	Arg	
					165					170					175		
15	ATG	TGG	AAC	CTC	ATT	GTG	CTT	TCC	TAT	GGC	TCC	AGC	TCA	CCA	GCC	CTG	576
	Met	Trp	Asn	Leu	Ile	Val	Leu	Ser	Tyr	Gly	Ser	Ser	Ser	Pro	Ala	Leu	
				180					185					190			
20	TCA	AAC	CGG	CAG	CGT	TTC	CCC	ACT	TTC	TTC	CGA	ACG	CAC	CCA	TCA	GCC	624
	Ser	Asn	Arg	Gln	Arg	Phe	Pro	Thr	Phe	Phe	Arg	Thr	His	Pro	Ser	Ala	
		195					200						205				
	ACA	CTC	CAC	AAC	CCT	ACC	CGC	GTG	AAA	CTC	TTT	GAA	AAG	TGG	GGC	TGG	672
25	Thr	Leu	His	Asn	Pro	Thr	Arg	Val	Lys	Leu	Phe	Glu	Lys	Trp	Gly	Trp	
		210					215					220					
	AAG	AAG	ATT	GCT	ACC	ATC	CAG	CAG	ACC	ACT	GAG	GTC	TTC	ACT	TCG	ACT	720
	Lys	Lys	Ile	Ala	Thr	Ile	Gln	Gln	Thr	Thr	Glu	Val	Phe	Thr	Ser	Thr	
30	225					230					235				240		
	CTG	GAC	GAC	CTG	GAG	GAA	CGA	GTG	AAG	GAG	GCT	GGA	ATT	GAG	ATT	ACT	768
	Leu	Asp	Asp	Leu	Glu	Glu	Arg	Val	Lys	Glu	Ala	Gly	Ile	Glu	Ile	Thr	
				245						250				255			
35	TTC	CGC	CAG	AGT	TTC	TTC	TCA	GAT	CCA	GCT	GTG	CCC	GTC	AAA	AAC	CTG	816
	Phe	Arg	Gln	Ser	Phe	Phe	Ser	Asp	Pro	Ala	Val	Pro	Val	Lys	Asn	Leu	
				260					265					270			
40	AAG	CGC	CAG	GAT	GCC	CGA	ATC	ATC	GTG	GGA	CTT	TTC	TAT	GAG	ACT	GAA	864
	Lys	Arg	Gln	Asp	Ala	Arg	Ile	Ile	Val	Gly	Leu	Phe	Tyr	Glu	Thr	Glu	
		275					280						285				

	GCC CGG AAA GTT TTT TGT GAG GTG TAC AAG GAG CGT CTC TTT GGG AAG	912
	Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys	
	290 295 300	
5	AAG TAC GTC TGG TTC CTC ATT GGG TGG TAT GCT GAC AAT TGG TTC AAG	960
	Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys	
	305 310 315 320	
10	ATC TAC GAC CCT TCT ATC AAC TGC ACA GTG GAT GAG ATG ACT GAG GCG	1008
	Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala	
	325 330 335	
15	GTG GAG GGC CAC ATC ACA ACT GAG ATT GTC ATG CTG AAT CCT GCC AAT	1056
	Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn	
	340 345 350	
20	ACC CGC AGC ATT TCC AAC ATG ACA TCC CAG GAA TTT GTG GAG AAA CTA	1104
	Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu	
	355 360 365	
25	ACC AAG CGA CTG AAA AGA CAC CCT GAG GAG ACA GGA GGC TTC CAG GAG	1152
	Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu	
	370 375 380	
30	GCA CCG CTG GCC TAT GAT GCC ATC TGG GCC TTG GCA CTG GCC CTG AAC	1200
	Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn	
	385 390 395 400	
35	AAG ACA TCT GGA GGA GGC GGC CGT TCT GGT GTG CGC CTG GAG GAC TTC	1248
	Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe	
	405 410 415	
40	AAC TAC AAC AAC CAG ACC ATT ACC GAC CAA ATC TAC CGG GCA ATG AAC	1296
	Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn	
	420 425 430	
45	TCT TCG TCC TTT GAG GGT GTC TCT GGC CAT GTG GTG TTT GAT GCC AGC	1344
	Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser	
	435 440 445	
50	GGC TCT CGG ATG GCA TGG ACG CTT ATC GAG CAG CTT CAG GGT GGC AGC	1392
	Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser	
	450 455 460	

	TAC AAG AAG ATT GGC TAC TAT GAC AGC ACC AAG GAT GAT CTT TCC TGG	1440
	Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp	
	465 470 475 480	
5	TCC AAA ACA GAT AAA TGG ATT GTT ATA TCC AGA ACT CAC AGC CCA ACC	1488
	Ser Lys Thr Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser Pro Thr	
	485 490 495	
10	TGA ACAACCTGAC TGCTGTGGGC TGCTCACTGG CTTTAGCTGC TGTCTTCCCC	1541
	*	
	CTGGGGCTCG ATGGTTACCA CATTGGGAGG AACCAGTTTC CTTTCGTCCTG CCAGGCCCCG	1601
15	CTCTGGCTCC TGGGCCCTGGG CTTTAGTCTG GGCTACGGTT CCATGTTTAC CAAGATTG	1661
	TGGGTCCACA CGGTCTTAC AAAGAAGGAA GAAAAGAAGG AGTGGAGGAA GACTCTGGAA	1721
20	CCCTGGAAGC TGTATGCCAC AGTGGGCCTG CTGGTGGGCA TGGATGTCCT CACTCTCGCC	1781
	ATCTGGCAGA TCGTGGACCC TCTGCACCGG ACCATTGAGA CATTGCCAA GGAGGAACCT	1841
	AAGGAAGATA TTGACGTCTC TATTCTGCCC CAGCTGGAGC ATTGCAGCTC CAGGAAGATG	1901
25	AATACATGGC TTGGCATTTC CTATGGTTAC AAGGGGCTGC TGCTGCTGCT GGGAATCTTC	1961
	CTTGCTTATG AGACCAAGAG TGTGTCCACT GAGAAGATCA ATGATCACCG GGCTGTGGGC	2021
30	ATGGCTATCT ACAATGTGGC AGTCCTGTGC CTCATCACTG CTCCTGTAC CATGATTCTG	2081
	TCCAGCCAGC AGGATGCAGC CTTTGCTTT GCCTCTCTTG CCATAGTTTT CTCCTCCTAT	2141
	ATCACTCTTG TTGTGCTCTT TGTGCCCAAG ATGCGCAGGC TGATCACCCG AGGGGAATGG	2201
35	CAGTCGGAGG CGCAGGACAC CATGAAGACA GGGTCATCGA CCAACAACAA CGAGGAGGAG	2261
	AAGTCCCGGC TGTGAGAGAA GGAGAACCGT GAACTGGAAA AGATCATTGC TGAGAAAGAG	2321
40	GAGCGTGTCT CTGAACTGCG CCATCAACTC CAGTCTCGGC AGCAGCTCCG CTCCCGGCGC	2381
	CACCCACCGA CACCCCCAGA ACCCTCTGGG GGCCTGCCCA GGGGACCCCC TGAGCCCCC	2441

GACCGGCTTA GCTGTGATGG GAGTCGAGTG CATTTGCTTT ATAAGTGA

2489

(2) INFORMATION FOR SEQ ID NO: 85:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 496 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

15 Met Leu Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
1 5 10 15

Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
20 25 30

20

Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
35 40 45

25 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
50 55 60

Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
65 70 75 80

30 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
85 90 95

Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val
100 105 110

35

Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp
115 120 125

40 Phe Arg Cys Asp Pro Asp Phe His Leu Cys Asp Pro Gly Gln Ala Thr
130 135 140

Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu
145 150 155 160

Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg
165 170 175

5 Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu
180 185 190

Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala
195 200 205

10 Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp
210 215 220

Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr
15 225 230 235 240

Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr
245 250 255

20 Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu
260 265 270

Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu
275 280 285

25 Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys
290 295 300

Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys
30 305 310 315 320

Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala
325 330 335

35 Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn
340 345 350

Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu
355 360 365

40 Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu
370 375 380

Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn
385 390 395 400

Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe
5 405 410 415

Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn
420 425 430

Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser
10 435 440 445

Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly Gly Ser
450 455 460

Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu Ser Trp
15 465 470 475 480

Ser Lys Thr Asp Lys Trp Ile Val Ile Ser Arg Thr His Ser Pro Thr
20 485 490 495

INTERNATIONAL SEARCH REPORT

International application No.

PCT/SE 98/01947

A. CLASSIFICATION OF SUBJECT MATTER

IPC6: C07K 14/705

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC6: C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SE,DK,FI,NO classes as above

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EMBL Databas Genbank/DDBJ, accession no. Y11044, Grifa A. et al: "GABA (gamma-amino-butyric acid)neurotransmission: identification and fine mapping of human GABA-B receptor gene"; Biochem. Biophys. Res. Commun. 250:240-245(1998) --	1-6,11-13, 16-26
X	Nature, Volume 386, March 1997, Klemens Kaupmann et al, "Expression cloning of GABAB receptors uncovers similarity to metabotropic glutamate receptors" page 239 - page 246 --	1-6,11-13, 16-26
X	WO 9746675 A1 (NOVARTIS AG), 11 December 1997 (11.12.97), page 50 - page 56, claim 4 --	1-6,11-13, 16-26

☒ Further documents are listed in the continuation of Box C.☒ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

23 March 1999

Date of mailing of the international search report

26-03-1999

Name and mailing address of the ISA

Swedish Patent Office

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/SE 98/01947

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	Dialog Information Services, File 34, SciSearch, Dialog accession no. 07157158, Goei VL et al: "Human gamma-aminobutyric acid B receptor gene: Complementary DNA cloning, expression, chromosomal location, and genomic organization", Biological Psychiatry, 1998, V44, N8(OCT 15), p659-666 --	1-6,11-13, 16-26
A	Brain Research Bulletin, Volume 38, No 6, 1995, Robert J. Washabau et al, "GABA Receptros in the Dorsal Motor Nucleus of the Vagus Influence Feline Lower Esophageal Sphincter and Gastric Function" page 587 - page 594 -- -----	1-6,11-13, 16-26

INTERNATIONAL SEARCH REPORT

International application No. _____

PCT/SE 98/01947

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See next page

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/SE 98/01947

According to PCT rule 13.2, an international application shall relate to one invention only or a group of inventions linked by one or more of the same or corresponding "special technical features", i.e. features that define a contribution which each of the inventions makes over the prior art.

The claimed invention relates to a nucleic acid sequence encoding a GABAB-receptor from either human or canine origin. A possible special technical features could have been nucleotide sequence encoding a GABAB-receptor. However a nucleotide sequence encoding a human GABAB-receptor is known from Grifa A. et. al., see the search report. Thus, the present application is considered to contain the following independent inventions:

Invention 1, claims 3-4, and the parts of claims 1-2 and 16-26 relating to claims 3-4: A human GABAB-receptor 1a, and related items,

Invention 2, claims 5-6, and the parts of claims 1-2 and 16-26 relating to claims 5-6: A human GABAB-receptor 1b, and related items,

Invention 3, claims 7-8, and the parts of claims 1-2 and 16-26 relating to claims 7-8: A human GABAB-receptor 1c, and related items,

Invention 4, claims 9-10, and the parts of claims 1-2 and 16-26 relating to claims 9-10: A human GABAB-receptor 1d, and related items,

Invention 5, claims 12-13, and the parts of claims 1, 11 and 16-26 relating to claims 12-13: A canine GABAB-receptor 1a, and related items.

Invention 6, claims 14-15, and the parts of claims 1, 11 and 16-26 relating to claims 14-15: A canine GABAB-receptor 1c, and related items.

The search has been limited to inventions 1, 2 and 5.

Information on patent family members

International application No.

PCT/SE 98/01947

Form PCT/ISA:210 (patent family annex) (July 1992)